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OM protein - protein search, using sw model

Run on: July 15, 2004, 23:48:38 ; Search time 77.2888 Seconds
(without alignments)

1089.410 Million cell updates/sec

Title: US-09-852-797-76

Perfect score: 1521

Sequence: 1 MARSRHRLLLLRLLVLA.....SSKATTMSDNFXHKSFI 298

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001s.*
- 5: Geneseq2002s.*
- 6: Geneseq2003as.*
- 7: Geneseq2003bs.*
- 8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1518	99.8	298	2	Aaw85457 Secreted
2	1518	99.8	298	4	Aau00512 Human jun
3	1518	99.8	298	5	Adp61801 Human pol
4	1518	99.8	298	6	Adr58532 Human vas
5	1517	99.7	298	2	Aaw75220 Human sec
6	1517	99.7	298	5	Aae26983 Human gen
7	1517	99.7	298	5	Aae27121 Human gen
8	1517	99.7	298	6	Abr47926 Human sec
9	1517	99.7	298	6	Abr00172 Human gen
10	1517	99.7	298	6	Abu64994 Human sec
11	1517	99.7	298	7	Abu91670 Human sec
12	1517	99.7	298	7	Adc74331 Human sec
13	1514	99.5	298	6	Aac16452 Human sec
14	1502.5	98.8	303	4	Aam23693 Human EST
15	1465	96.3	312	2	Aay23324 A33 relat
16	1465	96.3	312	2	Aay08060 Human PRO
17	1465	96.3	312	2	Aay13354 Amino aci
18	1465	96.3	312	3	Aab33421 Human PRO
19	1465	96.3	312	3	Aay70668 Human PRO
20	1465	96.3	312	3	Aab24401 Human PRO
21	1465	96.3	312	3	Adc78384 Human PRO
22	1465	96.3	312	4	AbB80222 Human PRO
23	1465	96.3	312	4	Aau08821 Human imm
24	1465	96.3	312	4	Aeu12339 Human PRO
25	1465	96.3	312	4	Aab53081 Human ang

26	1465	96.3	312	6	Abu71600 Human PRO
27	1465	96.3	312	6	Abol7783 Novel hum
28	1465	96.3	312	6	Abu71455 Human PRO
29	1465	96.3	312	6	Abu81037 Human PRO
30	1465	96.3	312	6	Abu71901 Human sec
31	1465	96.3	312	6	Abu01784 Novel hum
32	1465	96.3	312	6	Abu66737 Human PRO
33	1465	96.3	312	6	Abu54357 Human sec
34	1465	96.3	312	6	Abu47372 Human sec
35	1465	96.3	312	6	Abu59818 Novel sec
36	1465	96.3	312	6	Abu25008 Human sec
37	1465	96.3	312	6	Abu64509 Human sec
38	1465	96.3	312	6	Abu67355 Human sec
39	1465	96.3	312	6	Abol14875 Human sec
40	1465	96.3	312	6	Abu07738 Human A-3
41	1465	96.3	312	6	Abu67013 Human sec
42	1465	96.3	312	6	Abu69632 Novel hum
43	1465	96.3	312	6	Abol14814 Human sec
44	1465	96.3	312	6	Ada45855 Novel hum
45	1465	96.3	312	6	Ada76286 Human PRO

ALIGNMENTS

RESULT 1
AAW85457
ID AAW85457 standard; protein; 298 AA.

XX AAW85457;

DT 25-FEB-1999 (first entry)

XX Secreted protein encoded by clone ct864_4.

XX Secreted protein; nutritional activity; immune stimulating; vaccine;
XX suppressing activity; haematopoiesis regulating activity;
XX tissue growth activity; activin; inhibin activity; chemotaxis;
XX chemokinetic activity; haemostasis; thrombolytic activity; receptor;
XX ligand; anti-inflammatory; cadherin; tumour invasion suppressor;
XX tumour inhibition; gene therapy.

OS Homo sapiens.

XX WO9842739-A2.

XX 01-OCT-1998.

XX 20-MAR-1998; 98WO-US005653.

XX 21-MAR-1997; 97US-00822167.

PR 19-MAR-1998; 98US-00044466.

XX (GEMY) GENETICS INST INC.

XX Jacobs K, McCoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;

PI Spaulding V, Agostino MJ;

XX WPI; 1998-609890/51.

DR N-PSDB; AAV82780.

XX New polynucleotides encoding secreted human proteins - derived from human
PT foetal brain, adult brain, foetal kidney, placenta or adult pineal gland
PT cDNA libraries.

XX Claim 17; Page 73-74; 113pp; English.

PS The present sequence represents a secreted protein. The polynucleotide
XX and secreted protein are predicted to have biological activities which
CC would make them suitable for treating, preventing or ameliorating medical
CC conditions in humans and animals, although no supporting data is given.
CC Suggested activities include nutritional activity, immune stimulating
CC (e.g. as vaccines) or suppressing activity, haematopoiesis regulating

Handwritten note:
No alignment
to be made
for this
entry

CC activity, tissue growth activity, activin/inhibin activity,
CC chemotactic/chemokinetic activity, haemostatic and thrombolytic activity,
CC receptor/ligand activity, anti-inflammatory activity, cadherin/tumour
CC invasion suppressor activity, and tumour inhibition activity (no data is
CC given in the specification to support these activities). The
CC polynucleotide is also stated to be useful for gene therapy
XX
SQ Sequence 298 AA;

Query Match 99.8%; Score 1518; DB 2; Length 298;
Best Local Similarity 99.3%; Pred. No. 1.1e-117;
Matches 296; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MARRSRHRLLLRLYLVALGYHKA YGFSAPKDDQVVTA YQEA ILLACKTPKKTYSR 60
DB 1 MARRSRHRLLLRLYLVALGYHKA YGFSAPKDDQVVTA YQEA ILLACKTPKKTYSR 60
QY 61 LEWKLGSRVSFVYVYQQTLOGDFKNRAEMIDFNIRKNVTRSDAGKYRCEVSAPSEGOQN 120
DB 61 LEWKLGSRVSFVYVYQQTLOGDFKNRAEMIDFNIRKNVTRSDAGKYRCEVSAPSEGOQN 120
QY 121 LEEDTVTLVLVAPVPSCVPSSALSGTVVELRCQKEGNPAPEYTWFKDGIRLLENPR 180
DB 121 LEEDTVTLVLVAPVPSCVPSSALSGTVVELRCQKEGNPAPEYTWFKDGIRLLENPR 180
QY 181 LGSQSTNSSYTNTKTGTLOFNTVSKLDTGEYSCARNVGYRCPGKRMQVDDLNSGI 240
DB 181 LGSQSTNSSYTNTKTGTLOFNTVSKLDTGEYSCARNVGYRCPGKRMQVDDLNSGI 240
QY 241 IAAVVVVALVTSVCGLGVCYAKRGYFSKETSFKQSNSSSKATTMSNDPKHTKSFII 298
DB 241 IAAVVVVALVTSVCGLGVCYAKRGYFSKETSFKQSNSSSKATTMSNDPKHTKSFII 298

RESULT 2
ID AAU00512 standard; protein; 298 AA.
XX AAU00512;
XX
DT 09-MAY-2001 (first entry)
XX Human junctional adhesion protein (JAM2).
DE
XX
XX Junctional adhesion protein; JAM2; cellular localisation;
KW cellular expression; immunoprecipitation; stroke; phosphorylation;
KW glycosylation; paracellular migration; inflammatory disease; arthritis;
KW asthma; rheumatoid arthritis; inflammatory bowel disease;
KW Crohn's disease.
XX
XX Homo sapiens.
EH Key Location/Qualifiers
FT Peptide 1..28 "Possible signal peptide #2"
FT Peptide 1..20 "Possible signal peptide #1"
FT Protein 21..298 "Possible mature JAM2 #1"
FT Protein 29..298 "Possible mature JAM2 #2"
FT Domain 237..254 "Transmembrane domain"
XX
XX WO200114404-A1.
PN
XX
XX 01-MAR-2001.
PD
XX
XX 23-AUG-2000; 2000WO-US023158.
PF
XX
XX 24-AUG-1999; 99US-0150459P.
PR
XX
XX (TEXA-) TEXAS BIOTECHNOLOGY CORP.

XX
PI Cunningham S, Trindad Arrate Barros M;
XX WPI; 2001-218425/22.
DR N-PSDB; AAS00512.
XX
PT Novel nucleic acids encoding human junctional adhesion protein useful for
PT producing antibodies that are suitable for therapeutic purposes.
XX
XX Claim 4; Page 46-47; 51pp; English.

PS The sequence represents a human junctional adhesion molecule 2 (JAM2).
XX The polynucleotide encoding the polypeptide is useful for recombinant
CC production of JAM-2 protein, which in turn is useful for the production
CC of antibodies. The antibodies may be used for probing cellular
CC localisation and/or expression of JAM2 in tissues under normal and
CC disease states, for immunoprecipitating JAM2 protein from cells and/or
CC stroke tissues to determine whether it is modified by glycosylation and
CC phosphorylation, and for determining JAM2 function. The antibodies
CC inhibit interaction of JAM2 with inflammatory cells or influences their
CC paracellular migration, and is therefore useful for alleviating
CC inflammatory diseases such as arthritis, asthma, rheumatoid arthritis,
CC inflammatory bowel disease and Crohn's disease
XX
SQ Sequence 298 AA;

Query Match 99.8%; Score 1518; DB 4; Length 298;
Best Local Similarity 99.3%; Pred. No. 1.1e-117;
Matches 296; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MARRSRHRLLLRLYLVALGYHKA YGFSAPKDDQVVTA YQEA ILLACKTPKKTYSR 60
DB 1 MARRSRHRLLLRLYLVALGYHKA YGFSAPKDDQVVTA YQEA ILLACKTPKKTYSR 60
QY 61 LEWKLGSRVSFVYVYQQTLOGDFKNRAEMIDFNIRKNVTRSDAGKYRCEVSAPSEGOQN 120
DB 61 LEWKLGSRVSFVYVYQQTLOGDFKNRAEMIDFNIRKNVTRSDAGKYRCEVSAPSEGOQN 120
QY 121 LEEDTVTLVLVAPVPSCVPSSALSGTVVELRCQKEGNPAPEYTWFKDGIRLLENPR 180
DB 121 LEEDTVTLVLVAPVPSCVPSSALSGTVVELRCQKEGNPAPEYTWFKDGIRLLENPR 180
QY 181 LGSQSTNSSYTNTKTGTLOFNTVSKLDTGEYSCARNVGYRCPGKRMQVDDLNSGI 240
DB 181 LGSQSTNSSYTNTKTGTLOFNTVSKLDTGEYSCARNVGYRCPGKRMQVDDLNSGI 240
QY 241 IAAVVVVALVTSVCGLGVCYAKRGYFSKETSFKQSNSSSKATTMSNDPKHTKSFII 298
DB 241 IAAVVVVALVTSVCGLGVCYAKRGYFSKETSFKQSNSSSKATTMSNDPKHTKSFII 298

RESULT 3
ID ABP61801 standard; protein; 298 AA.
XX ABP61801;
XX
DT 04-OCT-2002 (first entry)
XX Human polypeptide SEQ ID NO 155.
XX
XX Human; cytostatic; antithrombotic; antiarthritic; vulnary; analgesic;
KW antiinflammatory; antibacterial; immunosuppressive; antiparkinsonian;
KW neuroprotective; nootropic; osteopathic; haemostatic; vasotrophic;
KW antitumor; fungicide; antidiabetic; antisthmatic; antiallergic;
KW immunostimulant; antiparasitic; secreted protein; transmembrane protein;
KW cytokine; cell proliferation; cell differentiation; autoimmune disease;
KW stem cell; growth factor; nervous system disease; neuropathy;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease;
KW osteoporosis; severe combined immunodeficiency; SCID; infection;
KW multiple sclerosis; rheumatoid arthritis; gene therapy.
XX
XX Homo sapiens.

XX PN US2002065394-A1.
XX PD 30-MAY-2002.
XX PF 22-DEC-2000; 2000US-00745763.
XX PR 18-MAR-1998; 98US-00040963.
XX PA (JACO/) JACOBS K.
XX PA (MCCO/) MCCOY J. M.
XX PA (LAVA/) LAVALLIE E. R.
XX PA (COLL/) COLLINS-RACIE L. A.
XX PA (EVAN/) EVANS C.
XX PA (MERB/) MERBERG D.
XX PA (TREA/) TREACY M.
XX PA (SPAU/) SPAULDING V.
XX PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
XX PI Merberg D, Treacy M, Spaulding V;
XX DR N-PSDB; ABQ92017.
XX PS WPI; 2002-582343/62.
XX PT Novel secreted or transmembrane protein and polynucleotide encoding the
XX PT protein, useful for diagnosis and treatment of neurological disorders,
XX PT cancer, autoimmune diseases, bone disorders and lung or liver fibrosis.
XX PS Claim 54; Page 116-117; 284pp; English.
XX CC The invention relates to human secreted or transmembrane protein (I),
XX CC their fragments and is encoded by specific complementary deoxyribonucleic
XX CC acid (cDNA) inserts (II), where the protein is substantially free from
XX CC other mammalian proteins. (I) are useful for preventing, treating or
XX CC ameliorating a medical condition, especially immunological treatment or
XX CC prevention of tumours. (I) exhibits activity relating to angiogenesis,
XX CC cytokine, cell proliferation, cell differentiation, antiinflammatory,
XX CC stem cell growth factor activity and activin or inhibin-related
XX CC activities. (I) can be used to manipulate stem cells in culture to give
XX CC rise to neuroepithelial cells that can be used to augment or replace
XX CC cells damaged by illness, autoimmune disease, accidental damage or
XX CC genetic disorders. (I) induces the proliferation of neural cells and
XX CC regeneration of nerve and brain tissue and is useful for the treatment of
XX CC central and peripheral nervous system diseases and neuropathies, such as
XX CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX CC lateral sclerosis. (I) is involved in chemotactic or chemokinetic
XX CC activity, regulation of haematopoiesis and is useful for treating myeloid
XX CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
XX CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
XX CC tissue growth and in tissue repair, healing of burns, incisions, ulcers,
XX CC for treating osteoporosis, osteoarthritis, bone degenerative disorders or
XX CC periodontal disease. (I) is also useful for gut protection or
XX CC regeneration and treatment of lung or liver fibrosis, reperfusion injury
XX CC in various tissues, various immune deficiencies and disorders including
XX CC severe combined immunodeficiency (SCID), bacterial or fungal infections,
XX CC autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis,
XX CC diabetes mellitus, myasthenia gravis, allergic reactions and conditions,
XX CC such as asthma or other respiratory problems. (II) is useful to express
XX CC recombinant protein, as markers for tissues in which the corresponding
XX CC protein is preferentially expressed and in gene therapy. The present
XX CC sequence is that of a polypeptide of the invention
XX SQ Sequence 298 AA;
Query Match 99.8%; Score 1518; DB 5; Length 298;
Best Local Similarity 99.3%; Pred. No. 1.1e-117;
Matches 296; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MARRSRHLLLLRLYLVALGYKAYGFSAPKQQQVVAVYQEAIIACKTKPKTVXSR 60
DB 1 MARRSRHLLLLRLYLVALGYKAYGFSAPKQQQVVAVYQEAIIACKTKPKTVSSR 60
QY 61 LEWKILGRSVFVYQTLQDGNRAEMIDFNIRIKNVTSDAGKYRCEVAPSEQGN 120

Db 61 LEWKILGRSVFVYQTLQDGNRAEMIDFNIRIKNVTSDAGKYRCEVAPSEQGN 120
QY 121 LBEEDTVLEVLVAPVPSCEVPSSALSGTVVLRQCKEGNPAPEYTFKDGIRLLENPR 180
Db 121 LBEEDTVLEVLVAPVPSCEVPSSALSGTVVLRQCKEGNPAPEYTFKDGIRLLENPR 180
QY 181 LGSQSTNSSTYNTKTGTLQFNVTSKLDTGEYSCEARNVGYRRCPGKMQVDDLNISGI 240
Db 181 LGSQSTNSSTYNTKTGTLQFNVTSKLDTGEYSCEARNVGYRRCPGKMQVDDLNISGI 240
QY 241 IAAVWVALVISVCGGLGVCYAKRGYFSKTSFQKSNSSSKATTMSNDPKHTKSFII 298
Db 241 IAAVWVALVISVCGGLGVCYAKRGYFSKTSFQKSNSSSKATTMSNDPKHTKSFII 298
RESULT 4
ABR58532
ID ABR58532 standard; protein; 298 AA.
XX ABR58532;
AC ABR58532;
XX 09-JUL-2003 (first entry)
XX Human vascular endothelial junction-associated molecule protein.
DE Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
XX Heart disease; atherosclerosis; endometriosis.
XX Homo sapiens.
XX WO2003025138-A2.
XX 27-MAR-2003.
XX 17-SEP-2002; 2002WO-US029560.
XX 17-SEP-2001; 2001US-0323469P.
XX 20-SEP-2001; 2001US-0323887P.
XX 13-NOV-2001; 2001US-0350666P.
XX 08-FEB-2002; 2002US-0355145P.
XX 08-FEB-2002; 2002US-0355257P.
XX 12-APR-2002; 2002US-0372246P.
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX Afar D, Ariz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
XX Zlotnik A;
XX WPI; 2003-354600/33.
XX N-PSDB; ACC72652.
XX New genes that are up-regulated or down-regulated in cancers, useful as
XX markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
XX therapeutic targets for screening drugs for treating these diseases.
XX Claim 12; Page 149; 767pp; English.
XX The present invention describes an isolated nucleic acid molecule, which
XX comprises the sequence of any of the genes that are up-regulated or down-
XX regulated in specific cancers (e.g. about 1031 genes up-regulated in
XX acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
XX related gene nucleotide sequences which encode the proteins given in
XX ABR58521 to ABR58709. Also described: (1) determining the presence or
XX absence of a pathological cell in a patient; (2) an expression vector
XX comprising a nucleic acid molecule described above; (3) a host cell
XX comprising the vector; (4) an isolated polypeptide, which is encoded by
XX the nucleic acid; (5) an antibody that specifically binds the polypeptide
XX of (4); (6) specifically targeting a compound to a pathological cell in a
XX patient by administering to the patient the antibody above; and (7) a
XX drug screening assay. The nucleic acid is useful as diagnostic markers or
XX therapeutic targets. In particular, the nucleic acid is useful for
XX diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,

CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
 CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
 CC atherosclerosis and endometriosis. The nucleic acid is also useful in
 CC drug screening, particularly for identifying agents for treating these
 CC pathologies
 XX
 SQ Sequence 298 AA;

Query Match 99.8%; Score 1518; DB 6; Length 298;
 Best Local Similarity 99.3%; Pred. No. 1.1e-117; Indels 0; Gaps 0;
 Matches 296; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MARRSRHRLLLRLVVALGYHKAYGFSAPKDDQOVVAVXYQEAAILACKTPKKTVXSR 60
 DB 1 MARRSRHRLLLRLVVALGYHKAYGFSAPKDDQOVVAVXYQEAAILACKTPKKTVSSR 60

QY 61 LEWKLGSRVSFVYQQTLOGDFKNRAEMIDFNIRIKNVTSDAGKYRCEVSAPSEOGQN 120
 DB 61 LEWKLGSRVSFVYQQTLOGDFKNRAEMIDFNIRIKNVTSDAGKYRCEVSAPSEOGQN 120

QY 121 LEEDTIVTLVAVAPVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR 180
 DB 121 LEEDTIVTLVAVAPVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR 180

QY 181 LGSQSTNSSYTWTGTGLQFNVTSKLDTGEYSCEARNVGYRRCPCGKRMQVDDLNSGI 240
 DB 181 LGSQSTNSSYTWTGTGLQFNVTSKLDTGEYSCEARNVGYRRCPCGKRMQVDDLNSGI 240

QY 241 IAAVVVALVISVCGLGVCYAOBKGYFSKETSFOKSNSSSKATTMSSEDFKTKSFII 298
 DB 241 IAAVVVALVISVCGLGVCYAOBKGYFSKETSFOKSNSSSKATTMSSEDFKTKSFII 298

RESULT 5
 AAW75220
 ID AAW75220 standard; protein; 298 AA.
 AC AAW75220;
 XX
 DT 29-JAN-1999 (first entry)
 XX
 DE Human secreted protein encoded by gene 25 clone HTEEB42.
 KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 KW developmental abnormality; foetal deficiency; blood; allergy; renal;
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH FH
 FT Misc-difference 42 /label= unknown
 FT FT
 FT Misc-difference 58 /label= unknown
 FT FT
 XX
 FN WO9840483-A2.
 XX
 XX
 PD 17-SEP-1998.
 XX
 XX 12-MAR-1998; 98WO-US004858.
 XX
 PR 14-MAR-1997; 97US-0040710P.
 PR 14-MAR-1997; 97US-0040762P.
 PR 30-MAY-1997; 97US-0048100P.
 PR 30-MAY-1997; 97US-0048189P.
 PR 30-MAY-1997; 97US-0048357P.
 PR 30-MAY-1997; 97US-0050934P.
 PR 06-JUN-1997; 97US-0048970P.

PR 05-SEP-1997; 97US-0057765P.
 PR 19-DEC-1997; 97US-0068368P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
 PI Soppet DR, Gentz RL, Wei YF, Moore PA, Young PE, Greene JM;
 PI Ferrie AM;
 XX
 XX WPI; 1998-520811/44.
 DR N-PSDB; AAV34310.
 XX
 XX Isolated human poly:nucleotide(s) encoding secretory peptide(s) - used to
 PT develop products for the diagnosis and treatment of e.g. inflammation,
 PT cancers, CNS disorders or immune system disorders.
 XX
 PS Claim 1; Page 168-169; 201pp; English.
 XX
 CC This sequence represents a secreted human protein encoded by the gene
 CC clone detailed in the descriptor line. The gene can be used to generate
 CC fusion proteins by linking to the gene to a human immunoglobulin FC
 CC portion (e.g. AAV34277) for increasing the stability of the fused protein
 CC as compared to the human protein only. The invention relates to 28 novel
 CC genes and their fragments (nucleic acid sequences: AAV34286-V34325; amino
 CC acid sequences AAW75196-W75235) which are useful for preventing, treating
 CC or ameliorating medical conditions e.g. by protein or gene therapy. Also,
 CC pathological conditions can be diagnosed by determining the amount of the
 CC new polypeptides in a sample or by determining the presence of mutations
 CC in the new polynucleotides. Specific uses are described for each of the
 CC 28 polynucleotides, based on which tissues they are most highly expressed
 CC in (see AAV34286 for described uses)
 XX
 SQ Sequence 298 AA;

Query Match 99.7%; Score 1517; DB 2; Length 298;
 Best Local Similarity 100.0%; Pred. No. 1.3e-117;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARRSRHRLLLRLVVALGYHKAYGFSAPKDDQOVVAVXYQEAAILACKTPKKTVXSR 60
 DB 1 MARRSRHRLLLRLVVALGYHKAYGFSAPKDDQOVVAVXYQEAAILACKTPKKTVXSR 60

QY 61 LEWKLGSRVSFVYQQTLOGDFKNRAEMIDFNIRIKNVTSDAGKYRCEVSAPSEOGQN 120
 DB 61 LEWKLGSRVSFVYQQTLOGDFKNRAEMIDFNIRIKNVTSDAGKYRCEVSAPSEOGQN 120

QY 121 LEEDTIVTLVAVAPVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR 180
 DB 121 LEEDTIVTLVAVAPVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR 180

QY 181 LGSQSTNSSYTWTGTGLQFNVTSKLDTGEYSCEARNVGYRRCPCGKRMQVDDLNSGI 240
 DB 181 LGSQSTNSSYTWTGTGLQFNVTSKLDTGEYSCEARNVGYRRCPCGKRMQVDDLNSGI 240

QY 241 IAAVVVALVISVCGLGVCYAOBKGYFSKETSFOKSNSSSKATTMSSEDFKTKSFII 298
 DB 241 IAAVVVALVISVCGLGVCYAOBKGYFSKETSFOKSNSSSKATTMSSEDFKTKSFII 298

RESULT 6
 AAE26983
 ID AAE26983 standard; protein; 298 AA.
 XX
 AC AAE26983;
 XX
 DT 13-DEC-2002 (first entry)
 XX
 XX Human gene 25 encoded secreted protein HTEEB42, SEQ ID NO:76.
 DE
 KW Human; immunodeficiency; X-linked agammaglobulinaemia; septic shock;
 KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer;
 KW Grave's disease; diabetes mellitus; haematopoietic disorder; stroke;
 KW respiratory disorder; asthma; allergy; gastrointestinal disorder;
 KW

inflammatory bowel disease; neurodegenerative disorder; hepatitis;
Parkinson's disease; Alzheimer's disease; cardiovascular disorder;
atherosclerosis; myocarditis; renal disorder; fungicide; virucide;
hyperproliferative disorder; acute glomerulonephritis; tonsillitis;
respiratory disorder; rhinitis; sinusitis; neurological disease;
endocrine disorder; Addison's disease; reproductive system disorder;
endometriosis; vasotropic; vulnerable; cytostatic; nootropic; cardiant;
anti-HIV; tranquiliser; gout; antiparasitic.
Homo sapiens.
Key Location/Qualifiers
Peptide 1..22
Protein /label= Signal_peptide
23..298
Misc-difference 42 /note= "Human mature secreted protein"
/label= Unknown
/note= "Encoded by GWG"
Misc-difference 58
/label= Unknown
/note= "Encoded by TSC"
US200207287-A1.
20-JUN-2002.
11-MAY-2001; 2001US-00852659.
11-SEP-1998; 98US-00152060.
(RUBE/) RUBEN S M.
(ROSE/) ROSEN C A.
(LIYI/) LI Y.
(ZENG/) ZENG Z.
(KYAW/) KYAW H.
(FISC/) FISCHER C L.
(LIH/) LI H.
(SOPP/) SOPPET D R.
(GENT/) GENTZ R L.
(WEIY/) WEI Y.
(MOOR/) MOORE P A.
(YOUN/) YOUNG P E.
(GREE/) GREENE J M.
(FERR/) FERRIE A M.
Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
Ferrie AM;
WPI: 2002-598780/64.
N-PSDB; AAD44660.
Novel human secreted polypeptides and polynucleotides for diagnosing,
preventing, treating immune, hyperproliferative, cardiovascular,
neurological, reproductive disorders and identifying modulators of
therapeutic use.
Claim 11; Page 186; 209pp; English.
AAB44636-AAD44676 represent cDNAs corresponding to 28 human secreted
protein genes, and AAE26959-AAE26999 represent the proteins they encode.
AAE27000-AAE27025 represent human secreted protein fragments or their
variants. The secreted proteins and genes are useful for preventing,
treating or ameliorating medical conditions, e.g., by protein or gene
therapy. Specific uses are described for each of the 28 genes, based on
the tissues in which they are most highly expressed and include
developing products for the diagnosis or treatment of immunodeficiencies,
e.g., X-linked agammaglobulinemia, B cell immunodeficiencies, severe
combined immunodeficiencies, autoimmune disorders e.g., systemic lupus
erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune
thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome,
Grave's disease, diabetes mellitus, dermatitis, inflammatory conditions

including septic shock, sepsis, reperfusion injury, inflammatory bowel
disease, Crohn's disease, haematopoietic disorders, respiratory disorders
e.g., asthma and allergy, gastrointestinal disorders e.g., inflammatory
bowel disease, cancers e.g., gastric, ovarian, lung, liver, bladder and
breast), central nervous system (CNS) disorders e.g., ischaemic brain
injury and/or stroke, neurodegenerative disorders e.g., Parkinson's
disease and Alzheimer's disease, AIDS-related dementia and prion disease,
cardiovascular disorders e.g., myocarditis, arrhythmias, atherosclerosis,
inflammatory disorders e.g., hepatitis, gout, trauma, pancreatitis,
sarcoidosis and allogenic transplant rejection, blood-related disorder
(thrombosis, arterial thrombosis, atherosclerosis), hyperproliferative
disorders, respiratory disorders e.g. rhinitis, sinusitis, tonsillitis,
lung cancer, allergic disorders, pneumonitis, renal disorders, e.g. acute
glomerulonephritis, neurological diseases, liver disorders, endocrine
disorders e.g., hyperthyroidism, Addison's disease, hyperpituitarism,
CC infectious diseases and reproductive system disorders e.g. endometriosis.
XX The present sequence represents a human secreted protein of the invention
SQ Sequence 298 AA;
Query Match 99.7%; Score 1517; DB 5; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.3e-117;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARRSRHLLLLRLVVALGCHYKAYGFSAPKQOVVTAVYQEAAILACKTPKTVXR 60
DB 1 MARRSRHLLLLRLVVALGCHYKAYGFSAPKQOVVTAVYQEAAILACKTPKTVXR 60
QY 61 LEWKILGRSVFVYQCOTLQGDFKRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGN 120
DB 61 LEWKILGRSVFVYQCOTLQGDFKRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGN 120
QY 121 LEEDVTLEVLVAPVSPCEVFSALSGTVVBLRQDKEGNPAPYTFWKDGIRLLENPR 180
DB 121 LEEDVTLEVLVAPVSPCEVFSALSGTVVBLRQDKEGNPAPYTFWKDGIRLLENPR 180
QY 181 LGSQSTNSSTYTWNTKTGTLOFNTVSKLDGECYSCARNSVGRCFKEMQVDDLNISGI 240
DB 181 LGSQSTNSSTYTWNTKTGTLOFNTVSKLDGECYSCARNSVGRCFKEMQVDDLNISGI 240
QY 241 IAAVVVVALVISVCGLVGYCAQRKGYSKETSFKQSNSSSKATTSENDFKTKSFII 298
DB 241 IAAVVVVALVISVCGLVGYCAQRKGYSKETSFKQSNSSSKATTSENDFKTKSFII 298
RESULT 7
AAE27121
ID AAE27121 standard; protein; 298 AA.
XX
AC AAE27121;
XX
DT 13-DEC-2002 (first entry)
XX
DE Human gene 25 encoded secreted protein HTEB542, SEQ ID NO:76.
XX Human; secreted protein; autoimmune disease; hyperproliferative disorder;
KW rheumatoid arthritis; neoplasm; cerebrovascular disorder; angiogenesis;
KW cerebral ischaemia; cardiovascular disorder; nervous system disorder;
KW cardiac arrest; Alzheimer's disease; ocular disorder; wound healing;
KW infection; corneal infection; skin aging; food additive; preservative;
KW tissue regeneration; immunosuppressive; antiproliferative; cytostatic;
KW cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;
KW antibacterial; virucide; fungicide; ophthalmological; gene therapy;
KW vulnerable.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..22 /label= Signal_peptide
FT Protein 23..298
FT Misc-difference 42 /note= "Mature human secreted protein"
FT

FT FT /label= Unknown
FT FT /note= "Encoded by GWG"
FT Misc-difference 58
FT /label= Unknown
FT /note= "Encoded by TSC"
XX
PN US2002076756-A1.
XX
XX 20-JUN-2002.
XX
XX 11-MAY-2001; 2001US-00853161.
XX
XX 02-FEB-2001; 2001US-0265583P.
XX
XX (RUBE/) RUBEN S M.
XX (ROSE/) ROSEN C A.
XX (LIYI/) LI Y.
XX (ZENG/) ZENG Z.
XX (KYAW/) KYAW H.
XX (FISC/) FISCHER C L.
XX (LIH/) LI H.
XX (SOPP/) SOPPET D R.
XX (GENT/) GENTZ R L.
XX (WEI/) WEI Y.
XX (MOOR/) MOORE P A.
XX (YOUN/) YOUNG P E.
XX (GRE/) GREENE J M.
XX (FERR/) FERRIE A M.
XX
XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM;
XX
XX WPI: 2002-574454/51.
XX N-PSDB; AAD44878.
XX
XX New nucleic acid molecules encoding 28 human secreted proteins, useful
PI for diagnosing, preventing, treating or ameliorating medical conditions
PT and as food additives or preservatives.
XX
XX Claim 11; Page 186-187; 209pp; English.
XX
XX AAD44854-AAD44984 represent cDNAs corresponding to 28 human secreted
CC protein genes, and AAE27097-AAE27137 represent the proteins they encode.
CC AAE27138-AAE27164 represent human secreted protein fragments. The genes
CC and their corresponding secreted proteins are useful for preventing,
CC treating or ameliorating medical conditions, e.g., by protein or gene
CC therapy. Secreted protein sequences of the invention are useful for the
CC diagnosis or treatment of disorders such as autoimmune diseases (e.g.
CC rheumatoid arthritis), hyperproliferative disorders (e.g. neoplasms of
CC the breast or liver), cerebrovascular disorders (e.g. cerebral ischaemia,
CC angiogenesis), cardiovascular disorders (e.g. cardiac arrest), nervous
CC system disorders (e.g. Alzheimer's disease), infections caused by fungi,
CC bacteria and viruses and ocular disorders (e.g. corneal infection). The
CC polypeptides can also be used to aid wound healing and epithelial cell
CC proliferation, to prevent skin aging due to sunburn, to maintain organs
CC before transplantation, for supporting cell culture of primary tissues,
CC to regenerate tissues and in chemotaxis. They can also be used as food
CC additives or preservative to increase or decrease storage capabilities,
CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
CC and other nutritional components. The present sequence represents a human
XX secreted protein of the invention
XX
XX Sequence 298 AA;
XX
XX Query Match 99.7%; Score 1517; DB 5; Length 298;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-117;
XX Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MARRSRHRLLLLLLYLVVALGYHAYGFSAPKQOOVTVAXYQAILACKTPKTVXSR 60
XX
XX 1 MARRSRHRLLLLLLYLVVALGYHAYGFSAPKQOOVTVAXYQAILACKTPKTVXSR 60
XX

QY 61 LEWKKLGRSVFVYQOITLQGFKNRAEMIDENIRIKNVTSDAGKYCEVSAPSEQON 120
DB 61 LEWKKLGRSVFVYQOITLQGFKNRAEMIDENIRIKNVTSDAGKYCEVSAPSEQON 120
QY 121 LEBDVTTLVLVAPAVPSCEVPSSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR 180
DB 121 LEBDVTTLVLVAPAVPSCEVPSSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR 180
QY 181 LGSQSTNSSYTNKTTGTLQFNVTVSKLDTGEVSCBARNVGYRRCPGKRMQVDDNLINSGI 240
DB 181 LGSQSTNSSYTNKTTGTLQFNVTVSKLDTGEVSCBARNVGYRRCPGKRMQVDDNLINSGI 240
QY 241 IAAVVVVVALVISVCGLGVCYAQKRGYFSKETSFOKSNSSSKATTMSENDFKHTKSFII 298
DB 241 IAAVVVVVALVISVCGLGVCYAQKRGYFSKETSFOKSNSSSKATTMSENDFKHTKSFII 298
RESULT 8
ABR47926
ID ABR47926 standard; protein; 298 AA.
XX
XX ABR47926;
XX
XX 12-JUN-2003 (first entry)
XX
XX Human secreted protein, SEQ ID 817.
XX
XX Cardiant; antiarrhythmic; antiarteriosclerotic; vasotrophic; cytostatic;
XX vulnerable; antiinflammatory; nootropic; neuroprotective;
XX antiparkinsonian; gene therapy; human; cardiovascular disorder.
XX
XX Homo sapiens.
XX
XX WC200295010-A2.
XX
XX 28-NOV-2002.
XX
XX 19-MAR-2002; 2002WO-US009785.
XX
XX 21-MAR-2001; 2001US-0277340P.
XX
XX 19-JUL-2001; 2001US-0306171P.
XX
XX 13-NOV-2001; 2001US-0331287P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
XX
XX WPI; 2003-129429/12.
XX
XX Novel human secreted proteins, useful for detecting, preventing,
XX diagnosing, prognosticating, treating and/or ameliorating cardiovascular
XX disorders such as arthritis.
XX
XX Claim 13; SEQ ID NO 817; 1881pp; English.
XX
XX The present invention relates to novel human secreted proteins (ABR47633-
XX ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins
XX and their coding sequences are useful for the preparation of a diagnostic
XX or pharmaceutical composition for diagnosing or treating a cardiovascular
XX disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary
XX arteriosclerosis and myocardial ischaemia), neural disorders, immune
XX system disorders, muscular disorders, reproductive disorders,
XX gastrointestinal disorders, pulmonary disorders, renal disorders,
XX proliferative disorders and/or cancerous diseases and conditions, for
XX wound healing and epithelial cell proliferation, to treat inflammation or
XX infection, for treating thrombosis and arteriosclerosis, for treating or
XX preventing neural damage which occurs in neuronal disorders or
XX neurodegenerative conditions such as Alzheimer's disease and Parkinson's
XX disease, to enhance bone and periodontal regeneration and aid in tissue
XX transplants or bone grafts, to prevent skin aging or hair loss, to
XX stimulate growth and differentiation of haematopoietic cells and bone
XX marrow cells when used in combination with other cytokines, to maintain
XX organs before transplantation or for supporting cell culture of primary
XX

CC tissues, to increase or decrease differentiation or proliferation of
CC embryonic stem cells, or to modulate mammalian characteristics or
CC metabolism. Note: The sequence data for this patent was published in
CC electronic format and is available from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 298 AA;

Query Match 99.7%; Score 1517; DB 6; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.3e-117;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARRSRRLRLRLRLVVALGYHKAAGFAPKQDQVAVXYQEAAILACKTPKTVXSR 60
Db 1 MARRSRRLRLRLRLVVALGYHKAAGFAPKQDQVAVXYQEAAILACKTPKTVXSR 60

QY 61 LEWKILGRSVFVYQQTLOGDFKNRAEMIDFNIRIKNVTSDAGKYRCEVSAPSEQQN 120
Db 61 LEWKILGRSVFVYQQTLOGDFKNRAEMIDFNIRIKNVTSDAGKYRCEVSAPSEQQN 120

QY 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVELRCQDKEGNPAPETWFKDGRLLLENPR 180
Db 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVELRCQDKEGNPAPETWFKDGRLLLENPR 180

QY 181 LGSQSTNSSTYMTNTKTGLQFNTVSKLDTGEYSCEARNSVGYRRCPKRMQVDDLNI 240
Db 181 LGSQSTNSSTYMTNTKTGLQFNTVSKLDTGEYSCEARNSVGYRRCPKRMQVDDLNI 240

QY 241 IAAVVVALVISVGLGVCAQRKGYFSKETSFKSNSSSKATTMSNDPKHTKSFII 298
Db 241 IAAVVVALVISVGLGVCAQRKGYFSKETSFKSNSSSKATTMSNDPKHTKSFII 298

RESULT 9
ABR00172
ID ABR00172 standard; protein; 298 AA.

XX AC ABR00172;
XX DT 03-APR-2003 (first entry)
XX DE Human gene 162 encoded secreted protein HTEB42, SEQ ID NO:461.

XX KW Human; secreted protein; digestive disorder; gastrointestinal disorder;
KW mouth; oesophagus; stomach; small intestine; large intestine; liver;
KW biliary tract; pancreas; cancer; tumour; hyperproliferative disorder;
KW immune disorder; inflammation; infection; wound healing; drug screening;
KW chromosome identification; chromosome mapping; cytostatic; gene therapy;
KW antiinflammatory; immunosuppressive; vulnary; chromosome 21q21.2.

XX OS Homo sapiens.
XX FN WO200276488-A1.
XX PD 03-OCT-2002.
XX PF 19-MAR-2002; 2002WO-US008276.
XX PR 21-MAR-2001; 2001US-0277340P.
XX PR 19-JUL-2001; 2001US-0306171P.
XX PR 13-NOV-2001; 2001US-0331287P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Rosen CA, Ruben SM;
XX DR WPI; 2003-029900/02.
XX DR N-PSDB; ABZ71351.
XX XX New human secreted proteins and nucleic acids, useful for detecting,
PT preventing, diagnosing, prognosticating, treating and/or ameliorating
PT e.g. gastrointestinal diseases and disorders, or cancers.
XX

PS
XX
CC ABZ71130-ABZ71478 represent cDNAs corresponding to 178 human secreted
CC protein genes, and ABP00011-ABP00299 represent the proteins they encode.
CC ABZ71479-ABZ71540 represent human secreted protein genomic fragments. The
CC invention also encompasses antibodies specific for the secreted proteins,
CC the use of the secreted proteins in drug screening, and recombinant
CC vectors and host cells comprising a nucleic acid of the invention. The
CC secreted proteins, nucleic acids encoding them, antibodies or antibody
CC fragments specific for the secreted proteins, and modulators of protein
CC activity are useful for diagnosing, treating, ameliorating or preventing
CC digestive disorders. Such conditions include disorders of the mouth,
CC oesophagus, stomach, small intestine, large intestine, liver, biliary
CC tract and pancreas, and include cancers of these organs and tissues. The
CC secreted proteins and their nucleic acids may also be used in the
CC treatment of immune disorders, inflammation, infection,
CC hyperproliferative disorders, and to promote wound healing. Nucleic acids
CC of the invention may be used for chromosome identification, chromosome
CC mapping, in gene therapy, for identifying individuals from minute
CC biological samples, as hybridisation probes, and as molecular weight
CC markers. The present sequence represents a human secreted protein of the
CC invention
XX
SQ Sequence 298 AA;

Query Match 99.7%; Score 1517; DB 6; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.3e-117;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARRSRRLRLRLVVALGYHKAAGFAPKQDQVAVXYQEAAILACKTPKTVXSR 60
Db 1 MARRSRRLRLRLVVALGYHKAAGFAPKQDQVAVXYQEAAILACKTPKTVXSR 60

QY 61 LEWKILGRSVFVYQQTLOGDFKNRAEMIDFNIRIKNVTSDAGKYRCEVSAPSEQQN 120
Db 61 LEWKILGRSVFVYQQTLOGDFKNRAEMIDFNIRIKNVTSDAGKYRCEVSAPSEQQN 120

QY 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVELRCQDKEGNPAPETWFKDGRLLLENPR 180
Db 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVELRCQDKEGNPAPETWFKDGRLLLENPR 180

QY 181 LGSQSTNSSTYMTNTKTGLQFNTVSKLDTGEYSCEARNSVGYRRCPKRMQVDDLNI 240
Db 181 LGSQSTNSSTYMTNTKTGLQFNTVSKLDTGEYSCEARNSVGYRRCPKRMQVDDLNI 240

QY 241 IAAVVVALVISVGLGVCAQRKGYFSKETSFKSNSSSKATTMSNDPKHTKSFII 298
Db 241 IAAVVVALVISVGLGVCAQRKGYFSKETSFKSNSSSKATTMSNDPKHTKSFII 298

RESULT 10
ABU64994
ID ABU64994 standard; protein; 298 AA.
XX AC ABU64994;
XX DT 15-MAY-2003 (first entry)
XX DE Human secreted protein gene 25, protein.
XX DE Secreted protein; immunodeficiency; multiple sclerosis;
KW severe combined immunodeficiency; autoimmune disorder; cancer;
KW rheumatoid arthritis; diabetes mellitus; haematopoietic disorder;
KW inflammatory condition; septic shock; inflammatory bowel disease;
KW Crohn's disease; respiratory disorder; asthma; allergy; stroke;
KW gastrointestinal disorder; central nervous system disorder;
KW ischaemic brain injury; neurodegenerative disorder; Parkinson's disease;
KW Alzheimer's disease; cardiovascular disorder; atherosclerosis;
KW blood-related disorder; thrombosis; atherosclerosis; renal disorder;
KW hyperproliferative disorder; acute glomerulonephritis; Addison's disease;
KW endocrine disorder; liver disease; reproductive system disorder;
KW endometriosis; infectious disease; pancreatic disorder; vaccine;
KW wound repair; angiogenesis; lymphatic disorder; hair loss; body weight;

KW body height; hair colour; human.
 XX Homo sapiens.
 OS US2002172994-A1.
 XX 21-NOV-2002.
 XX 11-MAY-2001; 2001US-00852797.
 XX 14-MAR-1997; 97US-0040710P.
 PR 14-MAR-1997; 97US-0040762P.
 PR 30-MAY-1997; 97US-0048100P.
 PR 30-MAY-1997; 97US-0048189P.
 PR 30-MAY-1997; 97US-0048357P.
 PR 30-MAY-1997; 97US-0059334P.
 PR 06-JUN-1997; 97US-0048970P.
 PR 05-SEP-1997; 97US-0057765P.
 PR 19-DEC-1997; 97US-0068368P.
 PR 12-MAR-1998; 98WO-US004858.
 PR 11-SEP-1998; 98US-00152060.
 PR 02-FEB-2001; 2001US-0265583P.
 XX (RUBE/) RUBEN S M.
 PA (ROSE/) ROSEN C A.
 PA (LIY/) LI Y.
 PA (ZENG/) ZENG Z.
 PA (KYAW/) KYAW H.
 PA (FISC/) FISCHER C L.
 PA (LIH/) LI H.
 PA (SOPP/) SOPPET D R.
 PA (GENT/) GENTZ R L.
 PA (WEI/) WEI Y.
 PA (MOOR/) MOORE P A.
 PA (YOUN/) YOUNG P B.
 PA (GEE/) GREENE J M.
 PA (FERR/) FERRIE A M.
 XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
 PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PB, Greene JM;
 PI Ferrie AM;
 XX WPI: 2003-310989/30.
 DR N-PSDB; ABX96990.
 XX New human secreted polypeptides and polynucleotides for diagnosing,
 PT prognosing, preventing and treating immune, hyperproliferative, liver,
 PT kidney, reproductive disorders and for identifying modulators of
 PT therapeutic use.
 PS Claim 11; Page 186; 209pp; English.
 XX The invention relates to an isolated polypeptide comprising an amino acid
 CC sequence at least 95% identical to sequence of 28 human secreted
 CC proteins, their fragment, polypeptide domain, epitope, secreted form,
 CC variant, allelic variant, or species homologue, or the encoded sequence
 CC included in ATCC 97921 and 97922. Also included are the encoding nucleic
 CC acids, recombinant vectors, host cells, antibodies, and genes. The
 CC proteins and nucleic acids are useful for diagnosing, preventing,
 CC treating, prognosing or ameliorating a medical condition e.g.
 CC immunodeficiencies (e.g. X-linked agammaglobulinemia, B cell
 CC disorders (e.g. systemic erythematous, rheumatoid arthritis, multiple
 CC sclerosis, autoimmune thyroiditis, autoimmune haemolytic anaemia,
 CC Goodpasture's syndrome, Grave's disease, diabetes mellitus, dermatitis),
 CC haematopoietic disorders, inflammatory conditions (e.g. septic shock,
 CC sepsis, reperfusion injury, inflammatory bowel disease, Crohn's disease),
 CC respiratory disorders (e.g. asthma and allergy), gastrointestinal
 CC disorders, cancers (e.g. gastric, ovarian, lung, bladder, liver and
 CC breast), central nervous system (CNS) disorders (e.g. ischaemic brain
 CC injury and/or stroke, traumatic brain injury), neurodegenerative
 CC disorders (e.g. Parkinson's disease and Alzheimer's disease, AIDS-related
 CC dementia, and prion disease), cardiovascular disorders (e.g.

CC atherosclerosis, myocarditis, cardiovascular disease, and cardiopulmonary
 CC bypass complications), inflammation (e.g. hepatitis, gout, trauma,
 CC pancreatitis, sarcoidosis, dermatitis, allergic transplant rejection),
 CC blood-related disorders (thrombosis, arterial thrombosis),
 CC hyperproliferative disorders, renal disorders (e.g. acute
 CC glomerulonephritis), endocrine disorders (e.g. Addison's disease,
 CC hyperthyroidism, hypoparathyroidism), liver diseases and disorders,
 CC reproductive system disorders (e.g. endometriosis), infectious diseases,
 CC and pancreatic disorders. Many other diseases and disorders are listed in
 CC the specification. They also useful as a vaccine adjuvant. Further they
 CC are useful to enhance or inhibit complement mediated cell lysis, for
 CC stimulating wound and tissue repair, angiogenesis, and the repair of
 CC vascular or lymphatic diseases or disorders. They are also useful to
 CC prevent hair loss, to modulate mammalian characteristics such as body
 CC height, weight, hair colour, and to increase or decrease storage
 CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
 CC minerals, cofactors or other nutritional components. The proteins are
 CC also useful for identifying binding partners. The present sequence
 CC represents a secreted protein of the invention
 XX
 SQ Sequence 298 AA;
 Query Match 99.7%; Score 1517; DB 6; Length 298;
 Best Local Similarity 100.0%; Pred. No. 1.3e-117; Indels 0; Gaps 0;
 Matches 298; Conservative 0; Mismatches 0;
 QY 1 MARRSRHRLLLRLVLLVVALGYHAYGFSAPKQDVVAVYQYQAILACKTPKTVASR 60
 DB 1 MARRSRHRLLLRLVLLVVALGYHAYGFSAPKQDVVAVYQYQAILACKTPKTVASR 60
 QY 61 LEWKKLGRSVFVYQQTLLQDFKNRAEMIDFNIRKNVTRSDAGKYRCEVSAPSEQGN 120
 DB 61 LEWKKLGRSVFVYQQTLLQDFKNRAEMIDFNIRKNVTRSDAGKYRCEVSAPSEQGN 120
 QY 121 LEEDTVTLVLVAPVPSCEVPSSALSGLVQKDEGNPAPETWFKDGIIRLENPR 180
 DB 121 LEEDTVTLVLVAPVPSCEVPSSALSGLVQKDEGNPAPETWFKDGIIRLENPR 180
 QY 181 LGSQSTNSSTYNTKGTGLQFNVTSLKDTGEYSCFARNVSVYRCPGKRMQVDDNLSGI 240
 DB 181 LGSQSTNSSTYNTKGTGLQFNVTSLKDTGEYSCFARNVSVYRCPGKRMQVDDNLSGI 240
 QY 241 IAAVWVVALVISVCGLVGYCQKGYCFKSTSFQKSNSSSKATTMSNDFKHTKSFII 298
 DB 241 IAAVWVVALVISVCGLVGYCQKGYCFKSTSFQKSNSSSKATTMSNDFKHTKSFII 298
 RESULT 11
 ADB91670
 ID ADB91670 standard; protein; 298 AA.
 XX ADB91670;
 AC ADB91670;
 XX 04-DEC-2003 (first entry)
 DT Human secreted protein #SEQ ID 616.
 DE Secreted protein; gene therapy; antidiabetic; diabetes; human.
 XX Homo sapiens.
 OS WO2003004622-A2.
 PN 16-JAN-2003.
 PD 19-MAR-2002; 2002WO-US0008124.
 PF 21-MAR-2001; 2001US-0277340P.
 PR 19-JUL-2001; 2001US-0306171P.
 PR 13-NOV-2001; 2001US-0331287P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX

PI Rosen CA, Ruben SM;
 XX WPI; 2003-229407/22.
 XX Nucleic acid encoding a human secreted protein is useful in diagnosing or
 PT treating diabetes or conditions related to diabetes.
 XX
 XX Claim 3; SEQ ID NO 616; 1537pp; English.
 PS
 XX The invention relates to isolated nucleic acid molecules ADB91065-
 CC ADB91448 and ADB91835-ADB91911 encoding human secreted proteins ADB91449-
 CC ADB91834. Also disclosed is a recombinant vector comprising a
 CC polynucleotide of the invention, and a recombinant host cell comprising
 CC the recombinant vector. The polypeptide of the invention is useful in
 CC identifying a binding partner by contacting the polypeptide with a
 CC binding partner, and determining whether the binding partner increases or
 CC decreases activity of the polypeptide. The polypeptide, polynucleotide,
 CC antibody or its fragment, agonist or antagonist are useful for preparing
 CC a pharmaceutical composition for diagnosing or treating diabetes or
 CC conditions related to diabetes. The present sequence is that of the human
 CC immunoglobulin Fc portion used to generate fusion proteins, increasing
 CC the stability of the fused protein as compared to the secreted protein
 CC only. Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 298 AA;
 SQ
 Query Match 99.7%; Score 1517; DB 7; Length 298;
 Best Local Similarity 100.0%; Pred. No. 1.3e-117;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MARRSRHRLLLRLVLLVVALGYHKAQFSAKDDQVVTAVXYQEAAILACKTPKKTIXSR 60
 Db 1 MARRSRHRLLLRLVLLVVALGYHKAQFSAKDDQVVTAVXYQEAAILACKTPKKTIXSR 60
 QY 61 LEWKKLGRSVSFVYQQTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQN 120
 Db 61 LEWKKLGRSVSFVYQQTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQN 120
 QY 121 LEEDTTLVLELVAPVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTFWFKDGIRLLENPR 180
 Db 121 LEEDTTLVLELVAPVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTFWFKDGIRLLENPR 180
 QY 181 LGSQSTNSSTYNTTKTGLTFQNTVSKLDTGEYSCEARNSVGYRRCPCGRMQVDDLNI 240
 Db 181 LGSQSTNSSTYNTTKTGLTFQNTVSKLDTGEYSCEARNSVGYRRCPCGRMQVDDLNI 240
 QY 241 IAAVVVVALVISVCGLVGVCYAQRKGYFSKETSFOKSNSSSKATTMSNDPFKTKSFII 298
 Db 241 IAAVVVVALVISVCGLVGVCYAQRKGYFSKETSFOKSNSSSKATTMSNDPFKTKSFII 298
 RESULT 12
 ID ADC74331 standard; protein; 298 AA.
 XX
 XX ADC74331;
 AC
 XX 01-JAN-2004 (first entry)
 DT
 XX Human secreted protein - SEQ ID 964.
 DE
 XX antianemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid;
 KW antidiabetic; immunosuppressive; dermatologic; nephrotropic;
 KW antiparkinsonian; neuroprotective; neurotropic; antibacterial; virucide;
 KW fungicide; antiparasitic; antiarteriosclerotic; vulnery; cytostatic;
 KW haemopoietic; haematologic; anaemia; autoimmune disorder;
 KW rheumatoid arthritis; inflammation; Grave's disease; diabetes;
 KW systemic lupus erythematosus; glomerulonephritis; neurodegenerative;
 KW parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis;
 KW cancer; bacterial; viral; fungal; parasitic infection; Gene therapy;
 KW human.

XX Homo sapiens.
 OS
 XX WO2003038063-A2.
 PN
 XX 08-MAY-2003.
 PD
 XX 19-MAR-2002; 2002WO-US008277.
 PF
 XX 21-MAR-2001; 2001US-0277340P.
 PR 19-JUL-2001; 2001US-0306171P.
 PR 13-NOV-2001; 2001US-0331287P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 BA
 XX Rosen CA, Ruben SM;
 PI
 XX WPI; 2003-430516/40.
 DR N-PSDB; ABC73716.
 DR
 XX New human secreted polypeptide for diagnosing, preventing or treating
 PT hematopoietic or hematologic disorders (e.g. anemia), autoimmune
 PT disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or
 PT atherosclerosis).
 XX
 XX Claim 16; SEQ ID NO 964; 2272pp; English.
 PS
 XX The invention relates to a novel human secreted polypeptide comprising a
 CC defined sequence given in the specification. The polypeptide, nucleic
 CC acid molecule, antibody, agonist or antagonist of the invention may be
 CC useful for preparing a composition for diagnosing or treating a
 CC haemopoietic or haematologic disorder such as anaemia, autoimmune
 CC disorders such as rheumatoid arthritis, inflammation, Grave's disease,
 CC diabetes, systemic lupus erythematosus or glomerulonephritis,
 CC neurodegenerative disorders including Parkinson's disease and Alzheimer's
 CC disease, wounds and hyperproliferative disorders including
 CC atherosclerosis or cancer, as well as bacterial, viral, fungal or
 CC parasitic infections. The polypeptide may also be used during gene
 CC therapy procedures and for identifying a binding partner by contacting
 CC the polypeptide with a binding partner and determining whether the
 CC binding partner increases or decreases the activity of the polypeptide.
 CC The current sequence is that of the human secreted protein of the
 CC invention.
 XX
 SQ Sequence 298 AA;
 Query Match 99.7%; Score 1517; DB 7; Length 298;
 Best Local Similarity 100.0%; Pred. No. 1.3e-117;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MARRSRHRLLLRLVLLVVALGYHKAQFSAKDDQVVTAVXYQEAAILACKTPKKTIXSR 60
 Db 1 MARRSRHRLLLRLVLLVVALGYHKAQFSAKDDQVVTAVXYQEAAILACKTPKKTIXSR 60
 QY 61 LEWKKLGRSVSFVYQQTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQN 120
 Db 61 LEWKKLGRSVSFVYQQTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQN 120
 QY 121 LEEDTTLVLELVAPVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTFWFKDGIRLLENPR 180
 Db 121 LEEDTTLVLELVAPVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTFWFKDGIRLLENPR 180
 QY 181 LGSQSTNSSTYNTTKTGLTFQNTVSKLDTGEYSCEARNSVGYRRCPCGRMQVDDLNI 240
 Db 181 LGSQSTNSSTYNTTKTGLTFQNTVSKLDTGEYSCEARNSVGYRRCPCGRMQVDDLNI 240
 QY 241 IAAVVVVALVISVCGLVGVCYAQRKGYFSKETSFOKSNSSSKATTMSNDPFKTKSFII 298
 Db 241 IAAVVVVALVISVCGLVGVCYAQRKGYFSKETSFOKSNSSSKATTMSNDPFKTKSFII 298
 RESULT 13
 AA016452

ID AA016452 standard; protein; 298 AA.
 AC AA016452;
 XX
 DT 17-APR-2003 (first entry)
 DE Human junctional adhesion molecule 2 (hJAM2).
 KW Human; gene therapy; extracellular region; junctional adhesion molecules;
 KW hJAM; immune system disorder; immune deficiency; autoimmune disorder;
 KW inflammatory disorder; cancer; wound healing; cardiovascular disease;
 KW full-length membrane-bound hJAM protein.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..28
 FT Protein /label= Signal_peptide
 FT 29..298
 FT Domain /note= "Mature hJAM2"
 FT 29..236
 FT /note= "Extracellular domain; Specifically claimed
 FT region"
 XX
 PN WO2003008541-A2.
 XX
 PD 30-JAN-2003.
 XX
 PF 05-JUL-2002; 2002WO-US019800.
 XX
 PR 16-JUL-2001; 2001US-0305752P.
 PR 05-FEB-2002; 2002US-0354345P.
 XX
 PA (ELIL) LILLY & CO ELI.
 XX
 PI Heuer JG, Smith RC, Su EW;
 XX
 DR WPI; 2003-221848/21.
 DR N-PSDB; AAL51599.
 XX
 XX New extracellular human junctional adhesion molecule (hJAM) polypeptide,
 PT useful for treating an immune system disorder such as an immune
 PT deficiency or an inflammatory disorder, cancer, wound healing, or a
 PT cardiovascular disease.
 XX
 PS Disclosure; Fig 1; 131pp; English.
 XX
 XX The invention comprises the DNA and protein sequences of the
 CC extracellular region of human junctional adhesion molecules (hJAM). The
 CC extracellular hJAM DNA and protein sequences are useful in the treatment
 CC of immune system disorders (e.g. immune deficiency); autoimmune
 CC disorders; inflammatory disorders; cancer; wound healing; or a
 CC cardiovascular disease. The present amino acid sequence represents the
 CC full-length membrane-bound hJAM2 protein
 XX
 SQ Sequence 298 AA;
 Query Match 99.58; Score 1514; DB 6; Length 298;
 Best Local Similarity 99.04; Pred. No. 2.3e-117;
 Matches 295; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MARRSRRLRLLLRLYLVALGYHKGAFSPKDDQVWTAAXYQEAAILACKTPKKTVXSR 60
 DB 1 MARRSRRLRLLLRLYLVALGYHKGAFSPKDDQVWTAAXYQEAAILACKTPKKTVXSR 60
 QY 61 LEWKLGSRVSFVYQOTLQDGFKNRAEMIDFNIRIKNVTSDAGKYRCEVSPSEQQN 120
 DB 61 LEWKLGSRVSFVYQOTLQDGFKNRAEMIDFNIRIKNVTSDAGKYRCEVSPSEQQN 120
 QY 121 LEEDTVTLVLVAPVSPVSSALSGTVVELRCQDKEGNPAPEYTWFKDGRILLENPR 180
 DB 121 LEEDTVTLVLVAPVSPVSSALSGTVVELRCQDKEGNPAPEYTWFKDGRILLENPR 180

QY 181 LGSQSTNSSYTMNTKTGTLOFNTVSKLDTGEYSCFARNVGYRRCPGKRMQVDDLNISGI 240
 DB 181 LGSQSTNSSYTMNTKTGTLOFNTVSKLDTGEYSCFARNVGYRRCPGKRMQVDDLNISGI 240
 QY 241 IAAVVVVALVISVCGLVGYAQRKGYSKETSFOKSNSSSKATTMSENDFKHTKSFII 298
 DB 241 IAAVVVVALVISVCGLVGYAQRKGYSKETSFOKSNSSSKATTMSENDFKHTKSFII 298
 RESULT 14
 AAM23693
 ID AAM23693 standard; protein; 303 AA.
 XX
 AC AAM23693;
 XX
 DT 12-OCT-2001 (first entry)
 DE Human EST encoded protein SEQ ID NO: 1218.
 KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
 KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
 KW gene therapy; nutrition.
 XX
 OS Homo sapiens.
 XX
 PN WO200154477-A2.
 XX
 PD 02-AUG-2001.
 XX
 PF 25-JAN-2001; 2001WO-US002687.
 XX
 PR 25-JAN-2000; 2000US-00491404.
 PR 17-JUL-2000; 2000US-00617746.
 PR 03-AUG-2000; 2000US-00631451.
 PR 15-SEP-2000; 2000US-00663870.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
 PI Cao Y, Drmanac RA, Zhang J, Werhman T;
 DR WPI; 2001-476164/51.
 DR N-PSDB; AAH98352.
 XX
 XX Isolated polypeptide for treatment of diseases, diagnostics, raising
 PT antibodies and research use.
 PS Claim 20; Page 878-879; 1275pp; English.
 XX
 CC The present invention provides the protein and coding sequences of novel
 CC proteins from a variety of organisms, including human, dog, cat, horse,
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
 CC from the organism of interest. They can be used in diagnostics,
 CC forensics, gene mapping, identification of mutations, to assess
 CC biodiversity and for nutritional purposes. The present sequence is a
 CC protein of the invention
 XX
 SQ Sequence 303 AA;
 Query Match 98.8%; Score 1502.5; DB 4; Length 303;
 Best Local Similarity 97.4%; Pred. No. 2.1e-116;
 Matches 295; Conservative 1; Mismatches 2; Indels 5; Gaps 1;
 QY 1 MARRSRRLRLLLRLYLVALGYHKGAFSPKDDQVWTAAXYQEAAILACKTPKKTVXSR 60
 DB 1 MARRSRRLRLLLRLYLVALGYHKGAFSPKDDQVWTAAXYQEAAILACKTPKKTVXSR 60
 QY 61 LEWKLGSRVSFVYQOTLQDGFKNRAEMIDFNIRIKNVTSDAGKYRCEVSPSEQQN 120
 DB 61 LEWKLGSRVSFVYQOTLQDGFKNRAEMIDFNIRIKNVTSDAGKYRCEVSPSEQQN 120

QY 121 LEEDTVTLEVL-----VAPAVPCEVPSSALSGTVVVELRCQDKGPNAPETWFKDGIRL 175
DB 121 LEEDTVTLEVLGDVHVLAPAVPCEVPSSALSGTVVVELRCQDKGPNAPETWFKDGIRL 180
QY 176 LEMPRIGSQSTNSGYTMTNTGTLOENTVSKLDTGEYSCEARNVGVRCPCGKRMQVDDL 235
DB 181 LEMPRIGSQSTNSGYTMTNTGTLOENTVSKLDTGEYSCEARNVGVRCPCGKRMQVDDL 240
QY 236 NISGIIAAVVVALVSVCGLVGYAQRKGYSFKTSFQKSNSSSKATTMSSEDFKHKS 295
DB 241 NISGIIAAVVVALVSVCGLVGYAQRKGYSFKTSFQKSNSSSKATTMSSEDFKHKS 300
QY 296 FII 298
DB 301 FII 303

RESULT 15
AAV23324
ID AAV23324 standard; protein; 312 AA.

AC AAV23324;
XX 02-SEP-1999 (first entry)
DT A33 related antigen PRO245.
DE A33 related antigen; PRO301; PRO362; PRO245; inflammatory disease;
XX tumour.
KW Homo sapiens.
XX W09927098-A2.
XX 03-JUN-1999.
XX 20-NOV-1998; 98WO-US024855.
XX 21-NOV-1997; 97US-0066364P.
PR 20-MAR-1998; 98US-0078936P.
PR 17-SEP-1998; 98WO-US019437.
XX (GETH) GENENTECH INC.

PI Ashkenazi A, Fong S, Goddard A, Gurney AL, Napier MA, Tumas D;
PI Wood WI;

XX WPI; 1999-404743/34.
DR N-PSDB; AAX81770.
XX Antigen PRO301, PRO362 and PRO245 related to A33.

PT Example 3; Fig 11; 122pp; English.

XX The specification describes A33 related antigens PRO301, PRO362 and
CC PRO245. The methods and compositions of the invention are useful for the
CC treatment and diagnosis of inflammatory disease and tumours in mammals.
CC Such inflammatory diseases include of inflammatory bowel disease,
CC systemic lupus erythematosus, rheumatoid arthritis, juvenile chronic
CC arthritis, spondyloarthropathies, systemic sclerosis, scleroderma,
CC idiopathic inflammatory myopathies, dermatomyositis, polymyositis,
CC Sjogren's syndrome, systemic vacuolitis, sarcoidosis, autoimmune hemolytic
CC anemia, immune pancytopenia, paroxysmal nocturnal hemoglobinuria,
CC autoimmune thrombocytopenia, idiopathic thrombocytopenic purpura, immune-
CC mediated thrombocytopenia, thyroiditis, Grave's disease, Hashimoto's
CC thyroiditis, juvenile lymphocytic thyroiditis, atrophic thyroiditis,
CC diabetes mellitus, immune-mediated renal disease, glomerulonephritis,
CC tubulointerstitial nephritis, demyelinating diseases of the central and
CC peripheral nervous systems such as multiple sclerosis, idiopathic
CC polynuropathy, hepatobiliary diseases, infectious hepatitis A, B, C, D,
CC E, nonhepatotropic viruses, autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC inflammatory and fibrotic lung diseases, gluten-sensitive enteropathy,

CC Whipple's disease, autoimmune or immune-mediated skin diseases allergic
CC diseases of the lung such as eosinophilic pneumonias, idiopathic
CC pulmonary fibrosis and hypersensitivity pneumonitis transplantation
CC associated diseases disease. The present sequence represents PRO245
XX
SQ Sequence 312 AA;
Query Match 96.3%; Score 1465; DB 2; Length 312;
Best Local Similarity 99.3%; Pred. No. 2.8e-113;
Matches 286; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MARRSRHRLLLLLLRYLVVALGYHKAQVGFSAKQDQVVAVXYQBAAILACKTPKKTVASR 60
DB 1 MARRSRHRLLLLLLRYLVVALGYHKAQVGFSAKQDQVVAVXYQBAAILACKTPKKTVASR 60
QY 61 LEWKLGSRVSFVYVYQQTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQN 120
DB 61 LEWKLGSRVSFVYVYQQTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQN 120
QY 121 LEEDTVTLEVLVAPAVPCEVPSSALSGTVVVELRCQDKGPNAPETWFKDGIRLLENPR 180
DB 121 LEEDTVTLEVLVAPAVPCEVPSSALSGTVVVELRCQDKGPNAPETWFKDGIRLLENPR 180
QY 181 LGSQSTNSGYTMTNTGTLOENTVSKLDTGEYSCEARNVGVRCPCGKRMQVDDLNI 240
DB 181 LGSQSTNSGYTMTNTGTLOENTVSKLDTGEYSCEARNVGVRCPCGKRMQVDDLNI 240
QY 241 IAAVVVALVSVCGLVGYAQRKGYSFKTSFQKSNSSSKATTMSSE 288
DB 241 IAAVVVALVSVCGLVGYAQRKGYSFKTSFQKSNSSSKATTMSSE 288

Search completed: July 15, 2004, 23:52:46
Job time : 81.2888 secs

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QM protein - protein search, using sw model

Run on: July 15, 2004, 23:50:59 ; Search time 23.107 Seconds
(without alignments)
665.797 Million cell updates/sec

Title: US-09-852-797-76
Perfect score: 1521
Sequence: 1 MARRSRRLRLLLRLVVA.....SSKATTMSNDPKHTKSFII 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1517	99.7	298	4	US-09-152-060-76
2	1465	96.3	312	4	US-09-254-465A-9
3	1465	96.3	312	4	US-09-907-794A-64
4	1465	96.3	312	4	US-09-905-125A-64
5	1465	96.3	312	4	US-09-902-775A-64
6	481	31.6	310	4	US-09-907-794A-423
7	481	31.6	310	4	US-09-905-125A-423
8	481	31.6	310	4	US-09-902-775A-423
9	429	28.2	299	3	US-09-188-930-189
10	429	28.2	299	4	US-09-188-930-331
11	429	28.2	299	4	US-09-462-270-2
12	429	28.2	299	4	US-09-254-465A-1
13	429	28.2	299	4	US-09-312-283C-189
14	429	28.2	299	4	US-09-312-283C-331
15	429	28.2	299	4	US-09-907-794A-119
16	429	28.2	299	4	US-09-905-125A-119
17	429	28.2	299	4	US-09-902-775A-119
18	421	27.7	300	4	US-09-254-465A-10
19	399	26.2	260	4	US-09-254-465A-23
20	399	26.2	263	4	US-09-254-465A-25
21	271.5	17.9	205	4	US-09-462-270-4
22	231	15.2	270	4	US-09-254-465A-24
23	231	15.2	273	4	US-09-254-465A-26
24	231	15.2	319	1	US-08-597-495B-22
25	231	15.2	319	3	US-09-068-051A-22
26	231	15.2	319	4	US-09-336-536-67
27	231	15.2	319	4	US-09-254-465A-6

28	219	14.4	318	3	US-09-068-051A-32	Sequence 32, Appl
29	210	13.8	387	4	US-09-175-928-2	Sequence 2, Appl
30	202	13.3	390	2	US-08-979-424-1	Sequence 1, Appl
31	202	13.3	390	4	US-09-907-794A-39	Sequence 39, Appl
32	202	13.3	390	4	US-09-905-125A-39	Sequence 39, Appl
33	202	13.3	390	4	US-09-902-775A-39	Sequence 39, Appl
34	201.5	13.2	394	4	US-09-336-536-39	Sequence 29, Appl
35	200	13.1	341	4	US-09-336-536-29	Sequence 28, Appl
36	200	13.1	370	4	US-09-336-536-40	Sequence 40, Appl
37	196	12.9	365	4	US-08-979-424-3	Sequence 3, Appl
38	195.5	12.9	365	2	US-09-272-496-2	Sequence 2, Appl
39	195.5	12.9	365	3	US-08-928-383B-2	Sequence 2, Appl
40	191.5	12.6	365	3	US-08-336-536-42	Sequence 42, Appl
41	183	12.0	249	4	US-08-928-383B-23	Sequence 23, Appl
42	183	12.0	365	3	US-08-928-383B-24	Sequence 24, Appl
43	183	12.0	365	3	US-08-928-383B-26	Sequence 26, Appl
44	180	11.8	246	4	US-09-336-536-31	Sequence 31, Appl
45	178.5	11.7				

ALIGNMENTS

RESULT 1
US-09-152-060-76
; Sequence 76, Application US/09152060
; Patent No. G443230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003Pl.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 76
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (42)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (58)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-152-060-76

Query Match 99.7%; Score 1517; DB 4; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.1e-141;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Handwritten: K.P. p...
Handwritten: 1000

QY 1 MARRSRHRLLLRLVVALGYHKAQFSAKQDQVTVAVYQBAIACKTPKKTYSR 60
Db 1 MARRSRHRLLLRLVVALGYHKAQFSAKQDQVTVAVYQBAIACKTPKKTYSR 60
QY 61 LEWKLGSRVSFVYQOTLQGFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQN 120
Db 61 LEWKLGSRVSFVYQOTLQGFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQN 120
QY 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVLRQDKEGNPAPEYTWFKDGIRLLENPR 180
Db 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVLRQDKEGNPAPEYTWFKDGIRLLENPR 180
QY 181 LGSQSTNSYTNMTKTGLQFNTVSKLDTGEYSCEARNVGYRCPGKRMQVDDLINSGI 240
Db 181 LGSQSTNSYTNMTKTGLQFNTVSKLDTGEYSCEARNVGYRCPGKRMQVDDLINSGI 240
QY 241 IAAVVVALVISVCGLVGYAQRKGYFSKETSFOKSNSSSKATTMSSEDFXHTKSFI 298
Db 241 IAAVVVALVISVCGLVGYAQRKGYFSKETSFOKSNSSSKATTMSSEDFXHTKSFI 298

RESULT 2

US-09-254-465A-9
; Sequence 9, Application US/09254465A
; Patent No. 6410708
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Napier, Mary A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
; TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
; FILE REFERENCE: P12161(US)
; CURRENT APPLICATION NUMBER: US/09/254.465A
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: PCT/US98/24855
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: US 60/066,364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 60/078,936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: PCT/US98/19437
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 30
; SEQ ID NO 9
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-254-465A-9

Query Match 96.3%; Score 1465; DB 4; Length 312;
Best Local Similarity 99.3%; Pred. No. 1.6e-136;
Matches 286; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MARRSRHRLLLRLVVALGYHKAQFSAKQDQVTVAVYQBAIACKTPKKTYSR 60
Db 1 MARRSRHRLLLRLVVALGYHKAQFSAKQDQVTVAVYQBAIACKTPKKTYSR 60
QY 61 LEWKLGSRVSFVYQOTLQGFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQN 120
Db 61 LEWKLGSRVSFVYQOTLQGFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQN 120
QY 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVLRQDKEGNPAPEYTWFKDGIRLLENPR 180
Db 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVLRQDKEGNPAPEYTWFKDGIRLLENPR 180
QY 181 LGSQSTNSYTNMTKTGLQFNTVSKLDTGEYSCEARNVGYRCPGKRMQVDDLINSGI 240
Db 181 LGSQSTNSYTNMTKTGLQFNTVSKLDTGEYSCEARNVGYRCPGKRMQVDDLINSGI 240

Good date

QY 241 IAAVVVALVISVCGLVGYAQRKGYFSKETSFOKSNSSSKATTMSSEDFXHTKSFI 288
Db 241 IAAVVVALVISVCGLVGYAQRKGYFSKETSFOKSNSSSKATTMSSEDFXHTKSFI 288

RESULT 3

US-09-907-794A-64
; Sequence 64, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-794A-64

Query Match 96.3%; Score 1465; DB 4; Length 312;
Best Local Similarity 99.3%; Pred. No. 1.6e-136;
Matches 286; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MARRSRRLRLRLRLRLVVALGYHKAQFSAKQDQVVTAVYQEAAILACKTPKKTVXSR 60
Db 1 MARRSRRLRLRLRLRLVVALGYHKAQFSAKQDQVVTAVYQEAAILACKTPKKTVSSR 60

Qy 61 LEWKLGSRVSFVYQOTLQDGFKNRAEMIDFNIRIKNVTSDAGKYRCEVSPSEOGQN 120
Db 61 LEWKLGSRVSFVYQOTLQDGFKNRAEMIDFNIRIKNVTSDAGKYRCEVSPSEOGQN 120

Qy 121 LEEDTVTLVLVAPVSPCEVPSSALSGTVVLELRCQDKEGNAPEYTWFKDGIRLLENPR 180
Db 121 LEEDTVTLVLVAPVSPCEVPSSALSGTVVLELRCQDKEGNAPEYTWFKDGIRLLENPR 180

Qy 181 LGSQSTNSSYTMNTKTGLQFNTVSKLDTGEYSCEARNVGYRCPGKRMQVDDLNISGI 240
Db 181 LGSQSTNSSYTMNTKTGLQFNTVSKLDTGEYSCEARNVGYRCPGKRMQVDDLNISGI 240

Qy 241 IAAVVVALVISVCGLVGCYVQAKRGYFSKETSFOKSNSSSKATTMSN 288
Db 241 IAAVVVALVISVCGLVGCYVQAKRGYFSKETSFOKSNSSSKATTMSN 288

RESULT 4
US-09-905-125A-64
; Sequence 64, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-125A-64

Query Match 96.3%; Score 1465; DB 4; Length 312;
Best Local Similarity 99.3%; Pred. No. 1.6e-136;
Matches 286; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MARRSRRLRLRLRLRLVVALGYHKAQFSAKQDQVVTAVYQEAAILACKTPKKTVXSR 60
Db 1 MARRSRRLRLRLRLRLVVALGYHKAQFSAKQDQVVTAVYQEAAILACKTPKKTVSSR 60

Qy 61 LEWKLGSRVSFVYQOTLQDGFKNRAEMIDFNIRIKNVTSDAGKYRCEVSPSEOGQN 120
Db 61 LEWKLGSRVSFVYQOTLQDGFKNRAEMIDFNIRIKNVTSDAGKYRCEVSPSEOGQN 120

Qy 121 LEEDTVTLVLVAPVSPCEVPSSALSGTVVLELRCQDKEGNAPEYTWFKDGIRLLENPR 180
Db 121 LEEDTVTLVLVAPVSPCEVPSSALSGTVVLELRCQDKEGNAPEYTWFKDGIRLLENPR 180

Qy 181 LGSQSTNSSYTMNTKTGLQFNTVSKLDTGEYSCEARNVGYRCPGKRMQVDDLNISGI 240
Db 181 LGSQSTNSSYTMNTKTGLQFNTVSKLDTGEYSCEARNVGYRCPGKRMQVDDLNISGI 240

Qy 241 IAAVVVALVISVCGLVGCYVQAKRGYFSKETSFOKSNSSSKATTMSN 288
Db 241 IAAVVVALVISVCGLVGCYVQAKRGYFSKETSFOKSNSSSKATTMSN 288

RESULT 5
US-09-902-775A-64
; Sequence 64, Application US/09902775A
; Patent No. 668451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone

APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30959
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 64
LENGTH: 312
TYPE: PRT
ORGANISM: Homo sapiens
US-09-902-775A-64

Query Match 96.3%; Score 1465; DB 4; Length 312;
Best Local Similarity 99.3%; Pred. No. 1.6e-136;
Matches 286; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MARRSRHLLLLRLYLVALGYHAYGFSAPKDOQVVTVAXYQAEILACKTPKKTYSR 60
DB 1 MARRSRHLLLLRLYLVALGYHAYGFSAPKDOQVVTVAXYQAEILACKTPKKTYSR 60

QY 61 LEWKLGSRVSFVYQOTLQGDFFKNRAEMIDFNIRKNTVTRSDAGKYRCEVSAPSQGN 120
DB 61 LEWKLGSRVSFVYQOTLQGDFFKNRAEMIDFNIRKNTVTRSDAGKYRCEVSAPSQGN 120
QY 121 LEEDTVTLVLVAPVPSCVPSVSSALSGTVLRLCQDKEGNPAPEYTWFKDGIIRLEENR 180
DB 121 LEEDTVTLVLVAPVPSCVPSVSSALSGTVLRLCQDKEGNPAPEYTWFKDGIIRLEENR 180
QY 181 LGSQSTNSSYTMNTKTGTLOFNTVSKLDTGEVSCVSEARNVSVYRRCPCGKRMQVDDNLNISI 240
DB 181 LGSQSTNSSYTMNTKTGTLOFNTVSKLDTGEVSCVSEARNVSVYRRCPCGKRMQVDDNLNISI 240
QY 241 IAAVVVVALVISVCGLVGYAQRKGYFSKETSFOKNSSSSKATTMSEN 288
DB 241 IAAVVVVALVISVCGLVGYAQRKGYFSKETSFOKNSSSSKATTMSEN 288
RESULT 6
US-09-907-794A-423
Sequence 423, Application US/09907794A
Patent No. 6635468
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313

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; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-794A-423

Query Match      31.6%; Score 481; DB 4; Length 310;
Best Local Similarity 35.8%; Pred. No. 2.5e-39;
Matches 114; Conservative 60; Mismatches 116; Indels 28; Gaps 10;

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DB 1 MALRRPRLRLCARLPDPFLLLLFRGCLIG-----AVNLKSNRTPVVO--EFESVELSC 53

QY 51 -KTPKKTVXSRLWKKL-GRSVSFVYVYQOTLOGDFKNRAEMI-DFNIRIKNVTSDAGKY 107
DB 54 IITDSQTSDFRIEWKKIQDQTTVFFDNKIQDGLAGRAEILGKTSLKINVTNRDSALY 113

QY 108 RCEVAPSSEQQNLBEDTIVLEVLVAPVPSCEVPSSALSGTVVLELRCQKGNPAPEYT 167
DB 114 RCEVVARNDR-KEIDEIVIELTVQKVPVFCVCPKAVPVGKMATLHCQESGHPRPHYS 172

QY 168 WFKDGIILLENPLRGSQTSNNSYTNWTKTGLQFNVTYKLDTGCEYSCERNVGYRCPG 227
DB 173 WYRNDVPLPTDSRANPRFNSSFLNSETGTLVFTAVHKDDSGQYICIASNDAGSARCEE 232

QY 281 KATTMSNDKHTKSFII 298
DB 293 YIRDEGDFRHKSSFVI 310

RESULT 7
US-09-905-125A-423
; Sequence 423, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
```

Db	233	QEMEVYDLNIGGI	GGVLAVLALITL	GCAYRRGYFTNN	QDGEYKFKPDGVN	292
Qy	281	KATTMSNDP	GHTKSFII	298		
Db	293	YIRTEEGD	DFRHKSSFVI	310		

RESULT 8

RESOL 8
UIS-09-902-775A-423

US-03-502-775A-423

Sequence 423, Application US/09902775A
Patent No. 6686451
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Chiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: 10466-14

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; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-808-775A-423

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Query Match	31.6%;	Score	481;	DB	4;	Length	310;
Best Local Similarity	35.8%;	Pred.	No.	2.5e-39;			
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QY	51	-KTPKKT	VXSRLEWKL	-GRSV	FVYVYQ	TLOGD	CFKNRAEMI -DFNIRIKNVT
DB	54	LIITQS	TPSPRIE	WKKI	QDEQ	TYYV	FDNKIQGLAGRAEILGKTSKIWNVT
QY	108	RECV	APSE	QGNLB	EDT	VT	LEVLVAPAVP
DB	114	RC	EVVAR	NDR-KEI	DEI	BI	VELTQVQKPVTP
QY	168	WPKD	GIRL	LEN	PR	IGS	QSTNSSTYNTKTGTLOFTVSKLDTGEYSC
DB	173	WYRND	VPLPTD	SRAN	PR	FNSS	FHNLSEGTGLVFTAVHKDSSGYYCIASND
QY	228	KMQV	DD	LD	NI	SGII	AAVVVVALVIVSCGLGVCAQKGYF--SKE--TSFQ---
DB	233	Q	EME	VY	DL	NI	GIGIIGGLVVLAVLALITLIGICCAVRRGYFIN
QY	281	KATT	MS	END	F	KTK	SFII 298
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RESULT 9

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US-09-188-930-189
; Sequence 189, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Orrust, Rene
; APPLICANT: Murrison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 189
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (247)...(247)
; NAME/KEY: UNSURE
; LOCATION: (289)...(289)
US-09-188-930-189

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Query Match 28.2%; Score 429; DB 3; Length 299;
Best Local Similarity 34.2%; Pred. NO. 3.2e-34;
Matches 106; Conservative 50; Mismatches 126; Indels 28; Gaps 8;
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OM protein - protein search, using sw model

Run on: July 15, 2004, 23:54:34 ; Search time 64.5401 Seconds
(without alignments)
1443.181 Million cell updates/sec

Title: US-09-852-797-76

Perfect score: 1521

Sequence: 1 MAARRRHLRLLLRLVWA.....SSKATTMSNDPHTKTSFII 298

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Gapop 10.0 , Gapext 0.5

Searched: 1285345 seqs, 312560633 residues

Total number of hits satisfying chosen parameters: 1285345

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:

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- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
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- 15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1518	99.8	298	14	US-10-139-849-2
4	1518	99.8	298	14	US-10-192-791-2
5	1518	99.8	298	16	US-10-601-953-889
6	1517	99.7	298	9	US-09-853-161-76
7	1517	99.7	298	9	US-09-852-659A-76
8	1517	99.7	298	9	US-09-852-797-76
9	1517	99.7	298	12	US-10-058-993-76
10	1465	96.3	312	9	US-09-909-320-64
11	1465	96.3	312	9	US-09-909-0888-64
12	1465	96.3	312	9	US-09-905-291A-64
13	1465	96.3	312	9	US-09-953-499-9
14	1465	96.3	312	9	US-09-902-853-64
15	1465	96.3	312	9	US-09-907-824-64

16	1465	96.3	312	9	US-09-907-841-64
17	1465	96.3	312	10	US-09-904-011-64
18	1465	96.3	312	10	US-09-906-742-64
19	1465	96.3	312	10	US-09-906-838-64
20	1465	96.3	312	10	US-09-907-613-64
21	1465	96.3	312	10	US-09-907-942-64
22	1465	96.3	312	10	US-09-904-859-64
23	1465	96.3	312	10	US-09-909-204-64
24	1465	96.3	312	10	US-09-904-820-64
25	1465	96.3	312	10	US-09-904-786-64
26	1465	96.3	312	10	US-09-906-646-64
27	1465	96.3	312	10	US-09-906-700-64
28	1465	96.3	312	10	US-09-903-786-64
29	1465	96.3	312	10	US-09-902-903-64
30	1465	96.3	312	10	US-09-903-749A-64
31	1465	96.3	312	10	US-09-904-119-64
32	1465	96.3	312	10	US-09-904-356-64
33	1465	96.3	312	10	US-09-902-736-64
34	1465	96.3	312	10	US-09-907-794-64
35	1465	96.3	312	10	US-09-903-943-64
36	1465	96.3	312	10	US-09-904-462-64
37	1465	96.3	312	10	US-09-907-925-64
38	1465	96.3	312	10	US-09-902-892-64
39	1465	96.3	312	10	US-09-903-820-64
40	1465	96.3	312	10	US-09-905-056-64
41	1465	96.3	312	10	US-09-909-064-64
42	1465	96.3	312	10	US-09-904-853-64
43	1465	96.3	312	10	US-09-905-381-64
44	1465	96.3	312	10	US-09-905-088-64
45	1465	96.3	312	10	US-09-907-575-64

ALIGNMENTS

RESULT 1

US-09-745-763-38
; Sequence 38, Application US/09745763
; Patent No. US20020065394A1

GENERAL INFORMATION:

APPLICANT: Jacobs, Kenneth
McCoy, John M.
Lavallie, Edward R.
Collins-Racie, Lisa A.
Evans, Cheryl
Merberg, David
Treacy, Maurice
Spaulding, Vikki

TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES

NUMBER OF SEQUENCES: 219

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 CambridgePark Drive

CITY: Cambridge

STATE: MA

COUNTRY: U.S.A.

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/09/745,763

APPLICATION NUMBER: 18-Jun-2000

FILING DATE: 18-Jun-2000

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Sprunger, Suzanne A.

REGISTRATION NUMBER: 41,323

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8284

TELEFAX: (617) 876-5851

Hand date

<p>TELEPHONE: (650) 855-0555 TELEFAX: (650) 845-4166 INFORMATION FOR SEQ ID NO: 30: SEQUENCE CHARACTERISTICS: LENGTH: 298 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear IMMEDIATE SOURCE: LIBRARY: DUODNOT02 CLONE: 1704050 SEQUENCE DESCRIPTION: SEQ ID NO: 30 : US-09-799-777-30</p>	<p>Query Match 99.8%; Score 1518; DB 9; Length 298; Best Local Similarity 99.3%; Pred. No. 1.4e-135; Matches 296; Conservative 0; Mismatches 2; Indels 0; Gaps 0;</p>
<p>1 MARRSRHRLLLLLRYLVVALGYHKA YGFSAPKQQVVTA VYQEA I LACKT P KKT V XSR 60 1 MARRSRHRLLLLLRYLVVALGYHKA YGFSAPKQQVVTA VYQEA I LACKT P KKT V XSR 60 61 LEWKLG RSVSVVYQQTLQGD FKNRAEMIDFNIRIKNVT RSDAGKYRCEVSAPSEGGQN 120 61 LEWKLG RSVSVVYQQTLQGD FKNRAEMIDFNIRIKNVT RSDAGKYRCEVSAPSEGGQN 120 121 LEEDTVTLEVLVAPVSPCEVPSSALSGTVVLELRCQDKEGNPAPEYTWFKDGIRLLENPR 180 121 LEEDTVTLEVLVAPVSPCEVPSSALSGTVVLELRCQDKEGNPAPEYTWFKDGIRLLENPR 180 181 LGSQSTNSSYTNTKTGTLOFNTVSKLDTGEYSCEARN SVGYRCPGKRQVDDLNISGI 240 181 LGSQSTNSSYTNTKTGTLOFNTVSKLDTGEYSCEARN SVGYRCPGKRQVDDLNISGI 240 241 IAAVVVVALVISVCGLVGYAQRKGYSFKTSFKSNSSSKATTMSNDPFKHTKSFII 298 241 IAAVVVVALVISVCGLVGYAQRKGYSFKTSFKSNSSSKATTMSNDPFKHTKSFII 298</p>	<p>QY DB QY DB QY DB QY DB</p>
<p>RESULT 2 US-09-799-777-30 Sequence 30, Application US/0979977 Patent No. US20020091244A1 GENERAL INFORMATION: APPLICANT: Lal, Preeti Hillman, Jennifer L. Corley, Neil C. Guegler, Karl J. Baugh, Mariah Sather, Susan Shah, Purvi TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS NUMBER OF SEQUENCES: 154 CORRESPONDENCE ADDRESS: ADDRESSEE: INCYTE PHARMACEUTICALS, INC. STREET: 3174 PORTER DRIVE CITY: PALO ALTO STATE: CALIFORNIA COUNTRY: USA ZIP: 94304 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/799,777 FILING DATE: 06-Mar-2001 CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA: APPLICATION NUMBER: US/09/002,485 FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION: NAME: BILLINGS, LUCY J. REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PF-0459 US TELECOMMUNICATION INFORMATION:</p>	<p>QY DB QY DB QY DB QY DB</p>

TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-139-849-2

Query Match 99.8%; Score 1518; DB 14; Length 298;
Best Local Similarity 99.3%; Pred. No. 1.4e-135;
Matches 296; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MARRSRRLLLRLYLVALGKAYGFSAPKDDQVVTAVYQEAAILACKTPKKTVXSR 60
DB 1 MARRSRRLLLRLYLVALGKAYGFSAPKDDQVVTAVYQEAAILACKTPKKTVSSR 60
QY 61 LEWKLGSRVSFVYQQTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEOGQN 120
DB 61 LEWKLGSRVSFVYQQTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEOGQN 120
QY 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTFWFGDGIIRLLENPR 180
DB 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTFWFGDGIIRLLENPR 180
QY 181 LGSQSTNSSYTMNTKTGTQLQNTVSKLDTGEYSCEARNVGVYRRCPCGRMVDLNLISGI 240
DB 181 LGSQSTNSSYTMNTKTGTQLQNTVSKLDTGEYSCEARNVGVYRRCPCGRMVDLNLISGI 240
QY 241 IAAVVVVALVISVCGLVGVCYQAKRGYFSKETSFOKSNSSSKATTMSNDPKHTKSFII 298
DB 241 IAAVVVVALVISVCGLVGVCYQAKRGYFSKETSFOKSNSSSKATTMSNDPKHTKSFII 298

RESULT 4
US-10-192-791-2
; Sequence 2, Application US/10192791
; Publication No. US20030130166A1
; GENERAL INFORMATION:
; APPLICANT: Texas Biotechnology Corporation
; TITLE OF INVENTION: A Polynucleotide Encoding a Human Junctional Adhesion Protein (JA
; FILE REFERENCE: TX4542P0430
; CURRENT APPLICATION NUMBER: US/10/192,791
; CURRENT FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-192-791-2

Query Match 99.8%; Score 1518; DB 14; Length 298;
Best Local Similarity 99.3%; Pred. No. 1.4e-135;
Matches 296; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MARRSRRLLLRLYLVALGKAYGFSAPKDDQVVTAVYQEAAILACKTPKKTVXSR 60
DB 1 MARRSRRLLLRLYLVALGKAYGFSAPKDDQVVTAVYQEAAILACKTPKKTVSSR 60
QY 61 LEWKLGSRVSFVYQQTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEOGQN 120
DB 61 LEWKLGSRVSFVYQQTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEOGQN 120
QY 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTFWFGDGIIRLLENPR 180
DB 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTFWFGDGIIRLLENPR 180
QY 181 LGSQSTNSSYTMNTKTGTQLQNTVSKLDTGEYSCEARNVGVYRRCPCGRMVDLNLISGI 240
DB 181 LGSQSTNSSYTMNTKTGTQLQNTVSKLDTGEYSCEARNVGVYRRCPCGRMVDLNLISGI 240

QY 241 IAAVVVVALVISVCGLVGVCYQAKRGYFSKETSFOKSNSSSKATTMSNDPKHTKSFII 298
DB 241 IAAVVVVALVISVCGLVGVCYQAKRGYFSKETSFOKSNSSSKATTMSNDPKHTKSFII 298
RESULT 5
US-10-601-953-889
; Sequence 889, Application US/10601953
; Publication No. US20040077540A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven C.
; TITLE OF INVENTION: Compositions And Methods For Modulating Physiology Of Epithelial
; TITLE OF INVENTION: Junctional Adhesion Molecules For Enhanced Mucosal Delivery Of
; TITLE OF INVENTION: Therapeutic Compounds
; FILE REFERENCE: 02-0305
; CURRENT APPLICATION NUMBER: US/10/601,953
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: 60/392,512
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 889
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-601-953-889

Query Match 99.8%; Score 1518; DB 16; Length 298;
Best Local Similarity 99.3%; Pred. No. 1.4e-135;
Matches 296; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MARRSRRLLLRLYLVALGKAYGFSAPKDDQVVTAVYQEAAILACKTPKKTVXSR 60
DB 1 MARRSRRLLLRLYLVALGKAYGFSAPKDDQVVTAVYQEAAILACKTPKKTVSSR 60
QY 61 LEWKLGSRVSFVYQQTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEOGQN 120
DB 61 LEWKLGSRVSFVYQQTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEOGQN 120
QY 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTFWFGDGIIRLLENPR 180
DB 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTFWFGDGIIRLLENPR 180
QY 181 LGSQSTNSSYTMNTKTGTQLQNTVSKLDTGEYSCEARNVGVYRRCPCGRMVDLNLISGI 240
DB 181 LGSQSTNSSYTMNTKTGTQLQNTVSKLDTGEYSCEARNVGVYRRCPCGRMVDLNLISGI 240
QY 241 IAAVVVVALVISVCGLVGVCYQAKRGYFSKETSFOKSNSSSKATTMSNDPKHTKSFII 298
DB 241 IAAVVVVALVISVCGLVGVCYQAKRGYFSKETSFOKSNSSSKATTMSNDPKHTKSFII 298

Handwritten signature

RESULT 6
US-09-853-161-76
; Sequence 76, Application US/09853161
; Patent No. US20020076756A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P3
; CURRENT APPLICATION NUMBER: US/09/853,161
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14

; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 76
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (42)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (58)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-853-161-76

Query Match 99.7%; Score 1517; DB 9; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.8e-135;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARRSRRLRLLLRYLVVVALGYHKAQGSAPKQVQVTVAVXYQAEILACKTPKKTYSR 60
Db 1 MARRSRRLRLLLRYLVVVALGYHKAQGSAPKQVQVTVAVXYQAEILACKTPKKTYSR 60
QY 61 LEWKLGSRVSFVYQQTLQDGFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQN 120
Db 61 LEWKLGSRVSFVYQQTLQDGFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQN 120
QY 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVELRCQKGNPAPETWFKDGIIRLLENPR 180
Db 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVELRCQKGNPAPETWFKDGIIRLLENPR 180
QY 181 LGSQSTNSSYTNTKTGTQLQNTVSKLDTGEYSCEARNVGYRRCPCGKRMQVDDLNI 240
Db 181 LGSQSTNSSYTNTKTGTQLQNTVSKLDTGEYSCEARNVGYRRCPCGKRMQVDDLNI 240
QY 241 IAAVVVALVSVCGLVGYCAQKGYFSKTSFQKSNSSSKATTMSNDFFKHTKSFII 298
Db 241 IAAVVVALVSVCGLVGYCAQKGYFSKTSFQKSNSSSKATTMSNDFFKHTKSFII 298

RESULT 7
US-09-852-659A-76
; Sequence 76, Application US/09852659A
; Patent No. US2002007287A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P4
; CURRENT APPLICATION NUMBER: US/09/852,659A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762

; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 76
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (42)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (58)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-852-659A-76

Query Match 99.7%; Score 1517; DB 9; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.8e-135;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARRSRRLRLLLRYLVVVALGYHKAQGSAPKQVQVTVAVXYQAEILACKTPKKTYSR 60
Db 1 MARRSRRLRLLLRYLVVVALGYHKAQGSAPKQVQVTVAVXYQAEILACKTPKKTYSR 60
QY 61 LEWKLGSRVSFVYQQTLQDGFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQN 120
Db 61 LEWKLGSRVSFVYQQTLQDGFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQN 120
QY 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVELRCQKGNPAPETWFKDGIIRLLENPR 180
Db 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVELRCQKGNPAPETWFKDGIIRLLENPR 180
QY 181 LGSQSTNSSYTNTKTGTQLQNTVSKLDTGEYSCEARNVGYRRCPCGKRMQVDDLNI 240
Db 181 LGSQSTNSSYTNTKTGTQLQNTVSKLDTGEYSCEARNVGYRRCPCGKRMQVDDLNI 240
QY 241 IAAVVVALVSVCGLVGYCAQKGYFSKTSFQKSNSSSKATTMSNDFFKHTKSFII 298
Db 241 IAAVVVALVSVCGLVGYCAQKGYFSKTSFQKSNSSSKATTMSNDFFKHTKSFII 298

RESULT 8
US-09-852-797-76
; Sequence 76, Application US/09852797
; Patent No. US20020172994A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P2
; CURRENT APPLICATION NUMBER: US/09/852,797
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858

APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909/320
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 64
LENGTH: 312
TYPE: PRT
ORGANISM: Homo sapiens
US-09-909-320-64

Query Match 96.3%; Score 1465; DB 9; Length 312;
Best Local Similarity 99.3%; Pred. No. 1.6e-130;
Matches 286; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MARRSRRLRLRLRLRVVVALGVHKAQFSAKDDQVTVAVYQEAAILACKTPKTVSR 60
Db 1 MARRSRRLRLRLRLRVVVALGVHKAQFSAKDDQVTVAVYQEAAILACKTPKTVSR 60
Qy 61 LEWKLGRSVSVFYQOITLQGFKNRAEMIDFNIRIKNVTNRSDAGKYRCEVAPSEQQN 120
Db 61 LEWKLGRSVSVFYQOITLQGFKNRAEMIDFNIRIKNVTNRSDAGKYRCEVAPSEQQN 120
Qy 121 LBDTDTLVLELVAPVPSCEVPSSALSGTVVLRQDKEGNAPEVTFKDGIRLLEMPR 180
Db 121 LBDTDTLVLELVAPVPSCEVPSSALSGTVVLRQDKEGNAPEVTFKDGIRLLEMPR 180
Qy 181 LGSQSTNSSYTMNTKTGTTLQFNVTSKLDTGEYSCEARNVSVYRRCPGKRMQVDDLNISGI 240
Db 181 LGSQSTNSSYTMNTKTGTTLQFNVTSKLDTGEYSCEARNVSVYRRCPGKRMQVDDLNISGI 240
Qy 241 IAAVVVVALVSVCGGLGVCYQKRGYFSKETSFKSNSSSKATTMSEN 288
Db 241 IAAVVVVALVSVCGGLGVCYQKRGYFSKETSFKSNSSSKATTMSEN 288
RESULT 11
US-09-909-088B-64
Sequence 64, Application US/09909088B
Patent No. US20020145709A1
GENERAL INFORMATION:
APPLICANT: Gerentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909/088B
CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089


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; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-088B-64

Query Match          96.3%; Score 1465; DB 9; Length 312;
Best Local Similarity 99.3%; Pred. No. 1.6e-130;
Matches 286; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MARRSRHRLLLRLYLVALGYHKAYGFSAPKDDQVVTAVYQEAAILACKTPKKTVXSR 60
Db 1 MARRSRHRLLLRLYLVALGYHKAYGFSAPKDDQVVTAVYQEAAILACKTPKKTVSSR 60

QY 61 LEWKLGSRVSFVYQOQTLOGDFKNRAEMIDFNIRKNVTRSDAGKYRCEVSAPSEQGN 120
Db 61 LEWKLGSRVSFVYQOQTLOGDFKNRAEMIDFNIRKNVTRSDAGKYRCEVSAPSEQGN 120

QY 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVLRCDKEGNPAPEYTWFKDGRIRLLENPR 180
Db 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVLRCDKEGNPAPEYTWFKDGRIRLLENPR 180

QY 181 LGSQSTNSSYTMNTKTGTLQFNVTSKLDTGEYSCARNVSVGYRRCPCGKRMQVDDLNI 240
Db 181 LGSQSTNSSYTMNTKTGTLQFNVTSKLDTGEYSCARNVSVGYRRCPCGKRMQVDDLNI 240

QY 241 IAAVVVVALVISVCGLGVCYAQRKGYSFKTSFKKSNSSSKATTMSN 288
Db 241 IAAVVVVALVISVCGLGVCYAQRKGYSFKTSFKKSNSSSKATTMSN 288

RESULT 12
US-09-905-291A-64
; Sequence 64, Application US/09905291A
; Patent No. US20020160374A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
```

```

; APPLICANT: Paoni, Nicholas F.
; APPLICANT: ROY, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905.291A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-291A-64

Query Match          96.3%; Score 1465; DB 9; Length 312;
Best Local Similarity 99.3%; Pred. No. 1.6e-130;
Matches 286; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MARRSRHRLLLRLYLVALGYHKAYGFSAPKDDQVVTAVYQEAAILACKTPKKTVXSR 60
Db 1 MARRSRHRLLLRLYLVALGYHKAYGFSAPKDDQVVTAVYQEAAILACKTPKKTVSSR 60

QY 61 LEWKLGSRVSFVYQOQTLOGDFKNRAEMIDFNIRKNVTRSDAGKYRCEVSAPSEQGN 120
Db 61 LEWKLGSRVSFVYQOQTLOGDFKNRAEMIDFNIRKNVTRSDAGKYRCEVSAPSEQGN 120

QY 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVLRCDKEGNPAPEYTWFKDGRIRLLENPR 180
Db 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVLRCDKEGNPAPEYTWFKDGRIRLLENPR 180

QY 181 LGSQSTNSSYTMNTKTGTLQFNVTSKLDTGEYSCARNVSVGYRRCPCGKRMQVDDLNI 240
Db 181 LGSQSTNSSYTMNTKTGTLQFNVTSKLDTGEYSCARNVSVGYRRCPCGKRMQVDDLNI 240

QY 241 IAAVVVVALVISVCGLGVCYAQRKGYSFKTSFKKSNSSSKATTMSN 288
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Db 241 TAAVVVALVISVGLGVCAQKRGYFSGKTSFQKSNSSSKATTMSEN 288
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RESULT 13

US-09-953-499-9
; Sequence 9, Application US/09953499
; Publication No. US20020182206A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Napier, Mary A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
; OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
; FILE REFERENCE: P1216R1(US)
; CURRENT APPLICATION NUMBER: US/09/953,499
; CURRENT FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: US/09/254,465
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: PCT/US98/24855
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: US 60/066,364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 60/078,936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: PCT/US98/19437
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 30
; SEQ ID NO 9
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-953-499-9

Query Match 96.3%; Score 1465; DB 9; Length 312;
Best Local Similarity 99.3%; Pred. No. 1.6e-130; Indels 0; Gaps 0;
Matches 286; Conservative 0; Mismatches 2

Qy 1 MARRSRRLRLRLRLVVALGYHKAQYFSGAPKDDQVVAVYQEAAILACKTKPKTVXSR 60
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Db 1 MARRSRRLRLRLRLVVALGYHKAQYFSGAPKDDQVVAVYQEAAILACKTKPKTVSSR 60
|||||

Qy 61 LEWKLGSRVSFVYVYQDTLQDGFKNRAEMIDFNIRIKNVTSDAGKYRCVSPSQGN 120
|||||

Db 61 LEWKLGSRVSFVYVYQDTLQDGFKNRAEMIDFNIRIKNVTSDAGKYRCVSPSQGN 120
|||||

Qy 121 LEEDTVLEVLVAVPVSCEVPVSALSGTVVLRCDQKGNPAPEYTWFKDGRLLLENPR 180
|||||

Db 121 LEEDTVLEVLVAVPVSCEVPVSALSGTVVLRCDQKGNPAPEYTWFKDGRLLLENPR 180
|||||

Qy 181 LGSOSTNSSTYMTNKTGTLQNTVSKLDTGEYCEARNVGYRCRCKRQVDDLNISGI 240
|||||

Db 181 LGSOSTNSSTYMTNKTGTLQNTVSKLDTGEYCEARNVGYRCRCKRQVDDLNISGI 240
|||||

Qy 241 TAAVVVALVISVGLGVCAQKRGYFSGKTSFQKSNSSSKATTMSEN 288
|||||

Db 241 TAAVVVALVISVGLGVCAQKRGYFSGKTSFQKSNSSSKATTMSEN 288
|||||

RESULT 14

US-09-902-853-64
; Sequence 64, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc

; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottitsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; ACIDS Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,853
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US/09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-902-853-64

Query Match 96.3%; Score 1465; DB 9; Length 312;
Best Local Similarity 99.3%; Pred. No. 1.6e-130; Indels 0; Gaps 0;
Matches 286; Conservative 0; Mismatches 2

Qy 1 MARRSRRLRLRLRLVVALGYHKAQYFSGAPKDDQVVAVYQEAAILACKTKPKTVXSR 60
|||||

Db 1 MARRSRHRLLLRLYLVALGYHKAQFSAKQDQVTVAVEYQEAAILACKTPKKTVSSR 60
QY 61 LEWKKLGRSVFVYQOTLQDGFKNRAEMIDFNIRIKNVTNRSDAGKYRCEVSAPSEQGN 120
Db 61 LEWKKLGRSVFVYQOTLQDGFKNRAEMIDFNIRIKNVTNRSDAGKYRCEVSAPSEQGN 120
QY 121 LEEDTVTLVLVAPVAPVSPVSSALSGTVELRCQDKEGNDPAPEYTWFKDGIRLLENPR 180
Db 121 LEEDTVTLVLVAPVAPVSPVSSALSGTVELRCQDKEGNDPAPEYTWFKDGIRLLENPR 180
QY 181 LGSQSTNSSYTMNTKTGLQFNVTVSKLDTGEYSCARNVGVYRRCQKRMQVDDDLNISI 240
Db 181 LGSQSTNSSYTMNTKTGLQFNVTVSKLDTGEYSCARNVGVYRRCQKRMQVDDDLNISI 240
QY 241 IAAVVVVVALVISVCGLVGCYQAQRKGYSKETSFKXSNSSSKATTMSEN 288
Db 241 IAAVVVVVALVISVCGLVGCYQAQRKGYSKETSFKXSNSSSKATTMSEN 288

RESULT 15

US-09-907-824-64
; Sequence 64, Application US/09907824
; Publication No. US20020197671A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,824
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089

; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
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; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-824-64

Query Match 96.3%; Score 1465; DB 9; Length 312;
Best Local Similarity 99.3%; Pred. No. 1.6e-130;
Matches 286; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MARRSRHRLLLRLYLVALGYHKAQFSAKQDQVTVAVEYQEAAILACKTPKKTVSSR 60
Db 1 MARRSRHRLLLRLYLVALGYHKAQFSAKQDQVTVAVEYQEAAILACKTPKKTVSSR 60
QY 61 LEWKKLGRSVFVYQOTLQDGFKNRAEMIDFNIRIKNVTNRSDAGKYRCEVSAPSEQGN 120
Db 61 LEWKKLGRSVFVYQOTLQDGFKNRAEMIDFNIRIKNVTNRSDAGKYRCEVSAPSEQGN 120
QY 121 LEEDTVTLVLVAPVAPVSPVSSALSGTVELRCQDKEGNDPAPEYTWFKDGIRLLENPR 180
Db 121 LEEDTVTLVLVAPVAPVSPVSSALSGTVELRCQDKEGNDPAPEYTWFKDGIRLLENPR 180
QY 181 LGSQSTNSSYTMNTKTGLQFNVTVSKLDTGEYSCARNVGVYRRCQKRMQVDDDLNISI 240
Db 181 LGSQSTNSSYTMNTKTGLQFNVTVSKLDTGEYSCARNVGVYRRCQKRMQVDDDLNISI 240
QY 241 IAAVVVVVALVISVCGLVGCYQAQRKGYSKETSFKXSNSSSKATTMSEN 288
Db 241 IAAVVVVVALVISVCGLVGCYQAQRKGYSKETSFKXSNSSSKATTMSEN 288

Search completed: July 16, 2004, 00:03:55
Job time : 66.5401 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	429	28.2	299	2	S56749		functional adhesio
2	201.5	13.2	365	2	JC3780		coxsackie- and ade
3	186	12.2	811	2	A41054		fasciadin II, tran
4	186	12.2	873	2	A41054		fasciadin II, PI-II
5	171	11.2	6642	2	T29757		protein UNC-89 - C
6	163.5	10.7	7962	2	I38346		elastic titin - hu
7	160.5	10.6	1367	2	A41228		protein-tyrosine k
8	157	10.3	344	2	A27681		non-specific cross-
9	157	10.3	860	2	JC5702		ErBb kinase activa
10	157	10.3	888	2	JC5701		ErBb kinase activa
11	156	10.3	1897	1	IDHULK		leukocyte antigen
12	155.5	10.2	1338	2	T23007		hypothetical prote
13	155.5	10.2	2783	2	T34416		hypothetical prote
14	155	10.2	725	2	JC5100		neural cell adhesi
15	155	10.2	850	2	JC5700		ErBb kinase activa
16	153.5	10.1	521	2	JC1508		biliary glycoprote
17	152	10.0	773	2	T46283		hypothetical prote
18	152	10.0	5175	2	T20992		hypothetical prote
19	152	10.0	5198	2	T43290		hemicentin precurs
20	151.5	10.0	1033	2	S19247		cell adhesion prot
21	151	9.9	1092	1	JN0635		neural cell adhesi
22	151	9.9	1501	2	I58148		protein-tyrosine-p
23	151	9.9	1863	2	S46217		protein-tyrosine-p
24	151	9.9	1898	2	S46216		leukocyte antigen-
25	150.5	9.9	521	2	S43338		biliary glycoprote
26	150	9.9	1499	2	I50312		protein-tyrosine-p
27	150	9.9	1907	2	S50893		protein-tyrosine-p
28	149.5	9.8	352	2	T33433		hypothetical prote
29	148.5	9.8	519	2	A44783		ecto-ATPase precu

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Dh 233 ERNVGVIIVAAVLVTLLILLGVFGIWFAYSRGHFDR---KKGTSSKKVIYQSPASRSEG 289
QY 289 DPKHTYSFII 298
Dh 290 EFKQTSSFLV 299

RESULT 2
JC7780
cox sackie- and adenovirus receptor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 02-Apr-2002
C:Accession: JC7780
R:Thoesen, I.; Keyvaerts, E.; Lindberg, M.; Van Ranst, M.
Biochem. Biophys. Res Commun. 288, 805-808, 2001
A:Title: Characterization of a cDNA encoding the bovine coxsackie and adenovirus recepto
A:Reference number: JC7780
A:Contents: Liver
A:Accession: JC7780
A:Molecule type: mRNA
A:Residues: 1-365 <THO>
A:Cross-References: GB:AY033651
C:Comment: This protein serves as the primary adenoviral attachment site on bovine cells

Query Match 13.2%; Score 201.5; DB 2; Length 365;
Best Local Similarity 24.5%; Pred. No. 1.2e-08;
Matches 78; Conservative 46; Mismatches 130; Indels 65; Gaps 11;

QY 12 LLRLVVALGVHKAAGSAPKQOVTVAVXQEAIIACK---TPKTVXSRLEW----- 63
Dh 3 LLRLFLLCGVADFRGLSITTPBQMIKAKGETAYLPCKFTPLGPEOGPLDIEWLLSPA 62

QY 64 --KKL-----GRSVFVYVYQTLQDGFKNRAEMI-----DFNIRIKNVTNRSDAGK 106
Dh 63 DNQKVDQVILYSGDKIYDDYQ-----DLKGRVFTSNLKGSGDASINVTNLQSLDGT 117

QY 107 YRCEV-SAPSEOGQNLBETVTLEVLVAPVPSCEVPSALSGLTVVELRCODKSGNPAPE 165
Dh 118 YQCKVKKAPGVGNKKIQ-----LTVLVRPSGIRCYVDGSEBIGNDFLKCPEKESLPLR 172

QY 166 YWFWKDGIRLLENPRGQSSTNSYTMNTKTGTQFNVTSKLDTGEVSCHEARNVGVYRRC 225
Dh 173 YEWQK-----LSDQKLPSTLWPEMTSPVISVKNASAEYSSTYCTVTRNVGSDQC 223

QY 226 -----PKRMQVDDLNISGIIAAVTVVALVSVGLGVCYAQKRGYFSKTSFQ--- 274
Dh 224 LLRLDVPFSPNRAGTIAGAVIGTLLALVLIALLIVFCCH-----KKRREEKYEYVHHDIR 279

QY 275 -----KSNSSSKATTMSEN 288
Dh 280 DVPPPKSTSTARSVIGSN 298

RESULT 3
A41054
fasciclin II, transmembrane splice form precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 17-Mar-2000
C:Accession: A41054
R:Grenningloh, G.; Rehm, E.J.; Goodman, C.S.
Cell 67, 45-57, 1991
A:Title: Genetic analysis of growth cone guidance in Drosophila: fasciclin II functions
A:Reference number: A41054; MUID:92005695; PMID:1913818
A:Accession: A41054
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-811 <GRE>
A:Cross-References: GB:M77165; NID:g157402; PID:g157403
C:Genetics:
A:Gene: FlyBase: Fas2
A:Cross-References: FlyBase: FBgn0000635
A:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C:Keywords: membrane protein

Query Match 12.2%; Score 186; DB 2; Length 811;
Best Local Similarity 24.6%; Pred. No. 5e-07;
Matches 67; Conservative 50; Mismatches 101; Indels 54; Gaps 13;

QY 30 SAPKQOVTVAVXQEAIIACKT---PKTVXSRLEWKKLG---BSVSFVYVYQTLQDGF 83
Dh 142 NAPENQYPTLG---QDYVVMCEVKADPNPTI---DWLRNGDPITRTNDKYVVOQT----- 189

QY 84 KNRAEMIDFNIRIKNVTNRSDAGKYRCEVSPSEOGQNLBETVTLEVLVAPVPSCEVPS 143
Dh 190 -----NGLLRNVQESDEGIYTCR-AAVETGELLER-TIRVEVFIQPEIISLPTNL 239

QY 144 SALSGLTVVELRCODKEGNPAPEYTFWKDGIIRLLENPRGQSSTNSYTMNTKTGTQLQNT 203
Dh 240 EAVEGKFPFAANTAR-GKVPVPEISWIRDATQL-----NVATADRQFQVNPOTGLVTISS 291

QY 204 VSKLDTGEVSCHEARNVGVYRRCPGK-----RMQVDDL-NISGIIAAVTVVALVSVCGLG 257
Dh 292 VSQDDYGTGTYTCLAKNRAGVVDQTKLNLVLRPQIYELYNVTGARTKEIAI----- 341

QY 258 VCYAQKGYFSKETSFOKSNSSSKATTMSEND 289
Dh 342 TCRA--KGRPAPAITFRWGTQEYVINGQDD 371

RESULT 4
B41054
fasciclin II PI-linked splice form precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 17-Mar-2000
C:Accession: B41054
R:Grenningloh, G.; Rehm, E.J.; Goodman, C.S.
Cell 67, 45-57, 1991
A:Title: Genetic analysis of growth cone guidance in Drosophila: fasciclin II functions
A:Reference number: A41054; MUID:92005695; PMID:1913818
A:Accession: B41054
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-873 <GRE>
A:Cross-References: GB:M77166
C:Genetics:
A:Gene: FlyBase: Fas2
A:Cross-References: FlyBase: FBgn0000635
A:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C:Keywords: transmembrane protein

Query Match 12.2%; Score 186; DB 2; Length 873;
Best Local Similarity 24.6%; Pred. No. 6e-07;
Matches 67; Conservative 50; Mismatches 101; Indels 54; Gaps 13;

QY 30 SAPKQOVTVAVXQEAIIACKT---PKTVXSRLEWKKLG---BSVSFVYVYQTLQDGF 83
Dh 142 NAPENQYPTLG---QDYVVMCEVKADPNPTI---DWLRNGDPITRTNDKYVVOQT----- 189

QY 84 KNRAEMIDFNIRIKNVTNRSDAGKYRCEVSPSEOGQNLBETVTLEVLVAPVPSCEVPS 143
Dh 190 -----NGLLRNVQESDEGIYTCR-AAVETGELLER-TIRVEVFIQPEIISLPTNL 239

QY 144 SALSGLTVVELRCODKEGNPAPEYTFWKDGIIRLLENPRGQSSTNSYTMNTKTGTQLQNT 203
Dh 240 EAVEGKFPFAANTAR-GKVPVPEISWIRDATQL-----NVATADRQFQVNPOTGLVTISS 291

QY 204 VSKLDTGEVSCHEARNVGVYRRCPGK-----RMQVDDL-NISGIIAAVTVVALVSVCGLG 257
Dh 292 VSQDDYGTGTYTCLAKNRAGVVDQTKLNLVLRPQIYELYNVTGARTKEIAI----- 341

QY 258 VCYAQKGYFSKETSFOKSNSSSKATTMSEND 289
Dh 342 TCRA--KGRPAPAITFRWGTQEYVINGQDD 371

RESULT 5
```

```
Dh 233 ERNVGVIIVAAVLVTLLILLGVFGIWFAYSRGHFDR---KKGTSSKKVIYQSPASRSEG 289
QY 289 DPKHTYSFII 298
Dh 290 EFKQTSSFLV 299

RESULT 2
JC7780
cox sackie- and adenovirus receptor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 02-Apr-2002
C:Accession: JC7780
R:Thoesen, I.; Keyvaerts, E.; Lindberg, M.; Van Ranst, M.
Biochem. Biophys. Res Commun. 288, 805-808, 2001
A:Title: Characterization of a cDNA encoding the bovine coxsackie and adenovirus recepto
A:Reference number: JC7780
A:Contents: Liver
A:Accession: JC7780
A:Molecule type: mRNA
A:Residues: 1-365 <THO>
A:Cross-References: GB:AY033651
C:Comment: This protein serves as the primary adenoviral attachment site on bovine cells

Query Match 13.2%; Score 201.5; DB 2; Length 365;
Best Local Similarity 24.5%; Pred. No. 1.2e-08;
Matches 78; Conservative 46; Mismatches 130; Indels 65; Gaps 11;

QY 12 LLRLVVALGVHKAAGSAPKQOVTVAVXQEAIIACK---TPKTVXSRLEW----- 63
Dh 3 LLRLFLLCGVADFRGLSITTPBQMIKAKGETAYLPCKFTPLGPEOGPLDIEWLLSPA 62

QY 64 --KKL-----GRSVFVYVYQTLQDGFKNRAEMI-----DFNIRIKNVTNRSDAGK 106
Dh 63 DNQKVDQVILYSGDKIYDDYQ-----DLKGRVFTSNLKGSGDASINVTNLQSLDGT 117

QY 107 YRCEV-SAPSEOGQNLBETVTLEVLVAPVPSCEVPSALSGLTVVELRCODKSGNPAPE 165
Dh 118 YQCKVKKAPGVGNKKIQ-----LTVLVRPSGIRCYVDGSEBIGNDFLKCPEKESLPLR 172

QY 166 YWFWKDGIRLLENPRGQSSTNSYTMNTKTGTQFNVTSKLDTGEVSCHEARNVGVYRRC 225
Dh 173 YEWQK-----LSDQKLPSTLWPEMTSPVISVKNASAEYSSTYCTVTRNVGSDQC 223

QY 226 -----PKRMQVDDLNISGIIAAVTVVALVSVGLGVCYAQKRGYFSKTSFQ--- 274
Dh 224 LLRLDVPFSPNRAGTIAGAVIGTLLALVLIALLIVFCCH-----KKRREEKYEYVHHDIR 279

QY 275 -----KSNSSSKATTMSEN 288
Dh 280 DVPPPKSTSTARSVIGSN 298

RESULT 3
A41054
fasciclin II, transmembrane splice form precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 17-Mar-2000
C:Accession: A41054
R:Grenningloh, G.; Rehm, E.J.; Goodman, C.S.
Cell 67, 45-57, 1991
A:Title: Genetic analysis of growth cone guidance in Drosophila: fasciclin II functions
A:Reference number: A41054; MUID:92005695; PMID:1913818
A:Accession: A41054
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-811 <GRE>
A:Cross-References: GB:M77165; NID:g157402; PID:g157403
C:Genetics:
A:Gene: FlyBase: Fas2
A:Cross-References: FlyBase: FBgn0000635
A:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C:Keywords: membrane protein

Query Match 12.2%; Score 186; DB 2; Length 811;
Best Local Similarity 24.6%; Pred. No. 5e-07;
Matches 67; Conservative 50; Mismatches 101; Indels 54; Gaps 13;

QY 30 SAPKQOVTVAVXQEAIIACKT---PKTVXSRLEWKKLG---BSVSFVYVYQTLQDGF 83
Dh 142 NAPENQYPTLG---QDYVVMCEVKADPNPTI---DWLRNGDPITRTNDKYVVOQT----- 189

QY 84 KNRAEMIDFNIRIKNVTNRSDAGKYRCEVSPSEOGQNLBETVTLEVLVAPVPSCEVPS 143
Dh 190 -----NGLLRNVQESDEGIYTCR-AAVETGELLER-TIRVEVFIQPEIISLPTNL 239

QY 144 SALSGLTVVELRCODKEGNPAPEYTFWKDGIIRLLENPRGQSSTNSYTMNTKTGTQLQNT 203
Dh 240 EAVEGKFPFAANTAR-GKVPVPEISWIRDATQL-----NVATADRQFQVNPOTGLVTISS 291

QY 204 VSKLDTGEVSCHEARNVGVYRRCPGK-----RMQVDDL-NISGIIAAVTVVALVSVCGLG 257
Dh 292 VSQDDYGTGTYTCLAKNRAGVVDQTKLNLVLRPQIYELYNVTGARTKEIAI----- 341

QY 258 VCYAQKGYFSKETSFOKSNSSSKATTMSEND 289
Dh 342 TCRA--KGRPAPAITFRWGTQEYVINGQDD 371

RESULT 4
B41054
fasciclin II PI-linked splice form precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 17-Mar-2000
C:Accession: B41054
R:Grenningloh, G.; Rehm, E.J.; Goodman, C.S.
Cell 67, 45-57, 1991
A:Title: Genetic analysis of growth cone guidance in Drosophila: fasciclin II functions
A:Reference number: A41054; MUID:92005695; PMID:1913818
A:Accession: B41054
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-873 <GRE>
A:Cross-References: GB:M77166
C:Genetics:
A:Gene: FlyBase: Fas2
A:Cross-References: FlyBase: FBgn0000635
A:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C:Keywords: transmembrane protein

Query Match 12.2%; Score 186; DB 2; Length 873;
Best Local Similarity 24.6%; Pred. No. 6e-07;
Matches 67; Conservative 50; Mismatches 101; Indels 54; Gaps 13;

QY 30 SAPKQOVTVAVXQEAIIACKT---PKTVXSRLEWKKLG---BSVSFVYVYQTLQDGF 83
Dh 142 NAPENQYPTLG---QDYVVMCEVKADPNPTI---DWLRNGDPITRTNDKYVVOQT----- 189

QY 84 KNRAEMIDFNIRIKNVTNRSDAGKYRCEVSPSEOGQNLBETVTLEVLVAPVPSCEVPS 143
Dh 190 -----NGLLRNVQESDEGIYTCR-AAVETGELLER-TIRVEVFIQPEIISLPTNL 239

QY 144 SALSGLTVVELRCODKEGNPAPEYTFWKDGIIRLLENPRGQSSTNSYTMNTKTGTQLQNT 203
Dh 240 EAVEGKFPFAANTAR-GKVPVPEISWIRDATQL-----NVATADRQFQVNPOTGLVTISS 291

QY 204 VSKLDTGEVSCHEARNVGVYRRCPGK-----RMQVDDL-NISGIIAAVTVVALVSVCGLG 257
Dh 292 VSQDDYGTGTYTCLAKNRAGVVDQTKLNLVLRPQIYELYNVTGARTKEIAI----- 341

QY 258 VCYAQKGYFSKETSFOKSNSSSKATTMSEND 289
Dh 342 TCRA--KGRPAPAITFRWGTQEYVINGQDD 371

RESULT 5
```


A:Reference number: A44476; MUID:93052339; PMID:1427854

A:Accession: E44476

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 35-141 <KHA>

A:Accession: F44476

A:Status: preliminary; not compared with conceptual translation

A:Residues: 35-137, 'L', 139-141 <KHZ>

C:Comment: this protein appears to be processed at the carboxyl terminus and anchored thru

C:Genetics:

A:Gene: GDB:NCA

A:Cross-references: GDB:120221; OMIM:163980

A:Map position: 19q13.2-19q13.2

A:Introns: 22/1

A:Note: the list of introns may be incomplete

C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-terminal

C:Keywords: blocked carboxyl end; glycoprotein; lipoprotein; membrane protein; phosphatic

F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>

F:1-34/Domain: signal sequence #status predicted <SIG>

F:35-320/Product: nonspecific cross-reacting antigen #status experimental <MAT>

F:160-217/Domain: immunoglobulin homology <IMW>

F:252-301/Domain: immunoglobulin homology <IMW2>

F:321-344/Domain: carboxyl-terminal propeptide #status predicted <CTP>

F:104,111,115,152,173,197,224,256,274,288,292/Binding site: carboxylate (Asn) (covalent)

F:309/Binding site: carboxylate (Asn) (covalent) #status predicted

F:320/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Gly) (in mature form)

Query Match 10.3%; Score 157; DB 2; Length 344;

Best Local Similarity 28.4%; Pred. No. 4.2e-05;

Matches 48; Conservative 25; Mismatches 62; Indels 34; Gaps 8;

QY 91 DFNRIKNVTSADGKYRCEVSAPSEQQNLEEDTVLELVAPAVSCVEPSSA--LSG 148

DB 197 NWTLLSVKRENDAGSECEIQNFSANRS---DPVILNVLVYGDGPITIS-PSKANVYRFG 252

QY 149 TVVELRCODKEGNPAPEYTWFKDGIIRLENPRLGQSQTNSSTYNTWTKTGLQFNTVSKLD 208

DB 253 ENLNLSCH-AAASNPAAQYSWPFING-----TFQOSTQELFIPNITVNN 293

QY 209 TGEVYSCEARNVGVYRCPG-KEMQVDDLNISG---IIAAVVVVVALVTSV 253

DB 294 SGSTWQCQHNH-----ATGLNRTVTMTVSSGAPVLSAVATVGTICV 337

RESULT 9

JCS702

E:BB kinase activator alpha2a, brain and thymus - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 25-Nov-1997 #sequence_revision 25-Nov-1997 #text_change 08-Sep-2002

C:Accession: JCS702; PC417

R:Hisaghiyama, S.; Horikawa, M.; Yamada, K.; Ichino, N.; Nakano, N.; Nakagawa, T.; Miyaguchi, J. Biochem. 122, 675-680, 1997

A:Title: A novel brain-derived member of the epidermal growth factor family that interacts with ErbB-2

A:Reference number: JCS700; MUID:98006324; PMID:9348101

A:Accession: JCS702

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-860 <HIG>

A:Cross-references: DBJ:J089996; NID:g2605631; PIDN:BAA23345.1; PID:g2605632

A:Experimental source: PC-12 cell

A:Accession: PC4417

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 'F', 212-213, 223-860 <HIG2>

A:Cross-references: DBJ:AB001576; NID:g2605478; PIDN:BAA23348.1; PID:g2605479

A:Experimental source: PC-12 cell

C:Comment: This protein is a member of the epidermal growth factor family. It is functionally related to the protein encoded by the MDA-MB-453 cells.

C:Superfamily: human ErbB kinase activator alpha, brain and thymus; EGF homology; immunoglobulin-like type 3

C:Keywords: glycoprotein

F:274-327/Domain: IG-like #status predicted <IGL>

F:361-397/Domain: EGF homology <EGF>

F;147,278,451/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.2%; Score 155; DB 2; Length 850;
Best Local Similarity 27.7%; Pred. No. 0.00018;
Matches 56; Conservative 24; Mismatches 86; Indels 36; Gaps 8;

Qy	66	LGRSVSFVYQQTLOGD--FKNRAEMIDFNIRIKNTVTRSDAGKYRCEVSAPSEQGNLEE	123
Db	188	LENRQYIFLEPTEQPLVFKTAPALDTN--GKNL-KKEVGKILCTDCATRPKLLKKMKS	244
Qy	124	DTVTLEVLVAPVPSCEVPSSALSGTVVELRCODKEGNPAPEYTWPKDGIRLLENPRLGS	183
Db	245	QTGQV-----GEKQSLKCEAAAGNFPQSYRWFPGDKELNR-----S	280
Qy	184	QSTNSSYTMNTKTGTLQFNVTVSKLDTGEYSCEARNVGYRRRCRPGKMQVDDLNI-----S	238
Db	281	RDIRIKYGNRKNRSLQFNKVKVEDAGEYVCEAENILGKDTVRG-RLYNVSVSTLLSSWS	339
Qy	239	GIIAVVVVVALVISVCGLGVCY	260
Db	340	GHARKCNETAKSYCVNG-GVCY	360

Search completed: July 15, 2004, 23:55:07
Job time : 24.3102 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2004, 23:49:03 ; Search time 12.7487 Seconds
(without alignments)
1217.140 Million cell updates/sec

Title: US-09-852-797-76
Perfect score: 1521
Sequence: 1 MARRSRHRLLLRLVVA.....SSKATMSNDPKTKTSFII 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1518	99.8	298	JAM2_HUMAN	P57087 homo sapien
2	429	28.2	299	JAM1_HUMAN	O9V624 homo sapien
3	421	27.7	300	JAM1_MOUSE	O88792 mus musculus
4	415.5	27.3	298	JAM1_BOVIN	Q9X556 bos taurus
5	231	15.2	319	A33_HUMAN	Q99795 homo sapien
6	195.5	12.9	365	CXAR_HUMAN	P78110 homo sapien
7	186	12.2	873	FAS2_DROME	P78110 drosophila
8	180	11.8	365	CXAR_MOUSE	P97792 mus musculus
9	171	11.2	6632	UN99_CABEL	O01761 caenorhabdi
10	164	10.8	344	CEA8_HUMAN	P40199 homo sapien
11	160.5	10.6	1367	VGR2_MOUSE	P35918 mus musculus
12	159.5	10.5	837	NMG2_MOUSE	O35136 mus musculus
13	157	10.3	868	NRG2_RAT	O35569 rattus norv
14	156	10.3	756	NRG2_MOUSE	P56974 mus musculus
15	155	10.3	1897	PTPF_HUMAN	P10586 homo sapien
16	155.5	10.2	837	NMG2_HUMAN	O15394 homo sapien
17	155	10.2	850	NRG3_HUMAN	O14511 homo sapien
18	153.5	10.1	521	CEA1_MOUSE	P31809 mus musculus
19	153.5	10.1	1343	VGR2_RAT	O08775 rattus norv
20	151	9.9	1092	NCA2_XENLA	P36335 xenopus lae
21	148.5	9.8	519	ECTO_RAT	P16573 rattus norv
22	148	9.7	1088	NCA1_XENLA	P16170 xenopus lae
23	148	9.7	1277	CAM1_FUGRU	Q98902 fugu rubrip
24	147.5	9.7	1091	NCA1_CHICK	P23590 gallus gall
25	147.5	9.7	1912	PTPD_HUMAN	P23468 homo sapien
26	147	9.7	526	CEA1_HUMAN	P13688 homo sapien
27	146.5	9.6	761	NCA2_HUMAN	P13592 homo sapien
28	146.5	9.6	848	NCA1_HUMAN	P13591 homo sapien
29	145	9.6	1051	PTK7_CHICK	O91048 gallus gall
30	145	9.5	333	AMAL_DROME	P15364 drosophila
31	145	9.5	764	ICCB_DROME	Q08180 drosophila
32	145	9.5	1302	NRG_DROME	P20241 drosophila
33	144.5	9.5	349	CEA8_HUMAN	P31957 homo sapien

34	143.5	9.4	1948	1	PTNS_HUMAN	Q13332 homo sapien
35	143	9.4	858	1	NCA1_RAT	P13596 rattus norv
36	142.5	9.4	265	1	CEA7_HUMAN	Q14002 homo sapien
37	140.5	9.2	344	1	NTRI_RAT	Q82713 rattus norv
38	140.5	9.2	847	1	CD22_HUMAN	P20273 homo sapien
39	140	9.2	359	1	LACH_DROME	Q24372 drosophila
40	140	9.2	853	1	NCA1_BOVIN	P18336 bos taurus
41	140	9.2	1906	1	KMLS_CHICK	P11799 gallus gall
42	140	9.2	4391	1	PGBM_HUMAN	P98160 homo sapien
43	139	9.1	725	1	NCA2_MOUSE	P13594 mus musculus
44	139	9.1	1115	1	NCA1_MOUSE	P13595 mus musculus
45	139	9.1	3707	1	PGBM_MOUSE	Q05793 mus musculus

ALIGNMENTS

RESULT 1
JAM2_HUMAN
ID JAM2_HUMAN STANDARD; PRT; 298 AA.
AC P57087;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Junctional adhesion molecule 2 precursor (Vascular endothelial
DE Junction-associated molecule) (VE-JAM).
GN JAM2 OR VEJAM OR C21ORF43.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Vascular endothelial cells;
RX MEDLINE=20317114; PubMed=10779521;
RA Palmeri D., van Zante A., Huang C.C., Hemmerich S., Rosen S.D.;
RT "Vascular endothelial junction-associated molecule, a novel member of
RT the immunoglobulin superfamily, is localized to intercellular
RT boundaries of endothelial cells.";
RL J. Biol. Chem. 275:19139-19145(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=20507930; PubMed=10945976;
RA Cunningham S.A., Arrate M.P., Rodriguez J.M., Bjerkke R.J.,
RT "A novel protein with homology to the junctional adhesion molecule:
RT Characterization of leukocyte interactions.";
RL J. Biol. Chem. 275:34750-34756(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

web data

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McWann P.J., McKernan K.J., Malek J.A., Gurnatne P.H.,
RA Villalón D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Maria M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -I- FUNCTION: Seems to play a role in epithelial tight junction
formation. Appears early in primordial forms of cell junctions and
recruits PARD3. The association of the PARD6-PARD3 complex may
prevent the interaction of PARD3 with JAM1, thereby preventing
tight junction assembly (By similarity). Plays a role in
regulating monocyte transmigration involved in integrity of
epithelial barrier. Involved in platelet activation.
CC -I- SUBUNIT: Interacts with the first PDZ domain of PARD3. The
association between PARD3 and PARD6B probably disrupts this
interaction (By similarity).
CC -I- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -I- TISSUE SPECIFICITY: Localized at tight junctions of both
epithelial and endothelial cells.
CC -I- SIMILARITY: Belongs to the immunoglobulin-like V-type domains.
CC -I- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
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CC EMBL; AF111713; AAD42050.1; -
CC EMBL; AF207907; AAF22829.1; -
CC EMBL; AF172398; AAD48877.1; -
CC EMBL; AL136649; CAB66594.1; -
CC EMBL; AY358896; AAO89255.1; -
CC EMBL; BC001533; AAO1533.1; -
CC PIR; A59406; S56749.
CC Genew; HGNC:14685; Fllr.
CC MIM; 605721; -
CC GO; GO:0005911; C:intercellular junction; TAS.
CC GO; GO:0006954; P:inflammatory response; TAS.
CC InterPro; IPR007110; IG-Like.
CC InterPro; IPR003596; IG_v.
CC Pfam; PF00047; Ig; 2.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS0835; IG Like; 2.
CC Tight junction; Immunoglobulin domain; Glycoprotein; Transmembrane;
KW Repeat; Signal.
KW SIGNAL 1 25
KW CHAIN 25
KW DOMAIN 26 299
KW TRANSMEM 239 299
KW DOMAIN 260 299
KW DOMAIN 27 125
KW DOMAIN 135 228
KW DISULFID 50 109
KW DISULFID 153 212
KW CARBOHYD 185 185
SQ SEQUENCE 299 AA; 32583 MW; D95DE2FEA23D2851 CRC64;
Query Match 28.2%; Score 429; DB 1; Length 299;
Best Local Similarity 34.2%; Pred. No. 5.4e-29;
Matches 106; Conservative 50; Mismatches 126; Indels 28; Gaps 8;
2 ARSRHRLLLRLVVLVVALGYHKAYGFSA-----PKDQVTVAVYQEAAILACKPKK 55

Db 5 AQVERKLLCLFILAILCLGSLAGSVTVHSSPEVRIPENNFVKLS CAYS-----GFSSP-- 58
QY 56 TVXSLEHK-KLGRSVSVVYQOTLQGFKNRAEMIDENIRIKNTRSDAGKYRCEVSAP 114
Db 59 ----RVEWKFQOGDTTRVLVCNNKITASYEDRVFLPTGIFKSVTRDTGTTCWVS-- 112
QY 115 SEQGONLEEDTVTLEVLVAPVPCEVPSALSGVTVELRCODKEGNPAPEYTFPKGIR 174
Db 113 EGGNSYGEVVKLVLPVPSKPTVNIPTSSATIGNRAVLTCSEODGSPSEYTFPKGIV 172
QY 175 LLENPLRSGQSTNSSTYNTTGTLOENTVSKLDTGEVSCARNSGVYRRCPGK-RMQVD 233
Db 173 MPTNPKSTRAFSSNSVYLNPTTGLVFLDLSASDTGEVSCARNGYGTFTMTSNVMEAV 232
QY 234 DLNIGIIIAAVVVAALVIVSGCLGVYQAKRGYFSKETSFKQSNSSSKA-----TTMSEN 288
Db 233 ERNVGVIAAVLVTLILGILVFGVWFAYSRGHEDRT---KKGTSKKVYSPQARSEG 289
QY 289 DPKHYSKFI 298
Db 290 EFKQTSSFLV 299
RESULT 3
JAM1_MOUSE STANDARD; PRT; 300 AA.
ID JAM1_MOUSE
AC O88792;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Functional adhesion molecule 1 precursor (JAM).
GN Fllr OR JAM1 OR JCAM1 OR JCAM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98327120; PubMed=9660867;
RA Martin-Padura I., Lostaglio S., Schneemann M., Williams L., Romano M.,
RA Fruscella P., Panzeri C., Stoppacciaro A., Ruco L., Villa A.,
RA Simons D., Dejana E.;
RT "Functional adhesion molecule, a novel member of the immunoglobulin
superfamily that distributes at intercellular junctions and modulates
monocyte transmigration.";
RT J. Cell Biol. 142:117-127(1998).
RN [2]
RP INTERACTION WITH PARD3.
RX MEDLINE=21340266; PubMed=11447115;
RA Ebnet K., Suzuki A., Horikoshi Y., Hirose T.,
RA Meyer zu Bruckwedde M.-K., Ohno S., Vestweber D.;
RT "The cell polarity protein ASIP/PAR-3 directly associates with
functional adhesion molecule (JAM).";
RT J. Cell Biol. 20:3738-3748(2001).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 212-238.
RX MEDLINE=21391702; PubMed=11500366;
RA Kostrewa D., Brockhaus M., D'Arcy A., Dale G.E., Nelboeck P.,
RA Schmid G., Mueller F., Bazzoni G., Dejana E., Bartfai T.,
RA Winkler F.K., Hennig M.;
RT "X-ray structure of functional adhesion molecule: structural basis for
homophilic adhesion via a novel dimerization motif.";
RL EMBO J. 20:4391-4398(2001).
CC -I- FUNCTION: Seems to play a role in epithelial tight junction
formation. Appears early in primordial forms of cell junctions and
recruits PARD3. The association of the PARD6-PARD3 complex may
prevent the interaction of PARD3 with JAM1, thereby preventing
tight junction assembly. Plays a role in regulating monocyte
transmigration involved in integrity of epithelial barrier.
CC Involved in platelet activation.
CC -I- SUBUNIT: Interacts with the first PDZ domain of PARD3. The
association between PARD3 and PARD6B probably disrupts this

```
CC interaction.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC Localized at tight junctions of both epithelial and endothelial
CC cells.
CC -!- TISSUE SPECIFICITY: Localized at tight junctions of both
CC epithelial and endothelial cells.
CC -!- SIMILARITY: Belongs to the immunoglobulin-like V-type domains.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U89915; AAC32982.1; -.
CC PDB; 1F97; 22-AUG-01.
CC MGI; 1321398; Flir.
CC GO; GO:0005515; f:protein binding; IPI.
CC InterPro; IPR007110; Ig-like.
CC Pfam; PF00047; Ig_2.
CC SMART; SM00406; Igv; 1.
CC PROSITE; PS50835; IG_LIKE; 2.
CC Tight junction; Immunoglobulin domain; Glycoprotein; Transmembrane;
CC Repeat; Signal; 3D-structure.
CC SIGNAL 1 26 POTENTIAL.
CC CHAIN 27 300 JUNCTIONAL ADHESION MOLECULE 1.
CC DOMAIN 27 238 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 239 259 POTENTIAL.
CC DOMAIN 260 299 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 28 122 IG-LOPE V-TYPE 1.
CC DOMAIN 134 230 IG-LIKE V-TYPE 2.
CC DISULFID 49 108 POTENTIAL.
CC DISULFID 152 212 POTENTIAL.
CC CARBOHYD 42 42 N-LINKED (GLCNAC...) (POTENTIAL).
CC CARBOHYD 185 185 N-LINKED (GLCNAC...) (POTENTIAL).
CC SEQUENCE 300 AA; 32368 MW; 391F3E48FF3B97EC CRC64;
CC -----
Query Match 27.7%; Score 421; DB 1; Length 300;
Best Local Similarity 34.6%; Pred. No. 2.6e-28;
Matches: 104; Conservative 55; Mismatches 130; Indels 12; Gaps 6;
QY 4 RSRRLRLLLRLVVALGYHKAYGFSAPKQDQVTVAVYQEAALLACKTPKKTVXSRLW 63
DB 6 KAGRKLLEFLTSMILGSLVQKGSVYTAQSDVQYPE-----NESIKLTCTYSGFSSPRVW 61
QY 64 KKL-GRSVSVFYVYQOTLQGDFFKRAEMIDFNIRIKNTRSDAGKYRCEVSAPSEQQNLE 122
DB 62 KVVQGSTTALVCYNSQITAPYADRVTFFSSGITTFFSVTRKDNGEYTCWVS--BEGGQNYG 119
QY 123 EDTVTLEVLVAPVPSCEPSSALSGTVLRLCODEKGNPAPEYTFKDGIRLLENPLRG 182
DB 120 EVSHLTVLVPPSTIVSPSSVIGRAVLTCSEHDSPPSEYVFKDGLISMLTADAKX 179
QY 183 SQS--TNSYTNWTKTQLQNTVSKLDTGEYSCBARNVSG-YRCPGKRVQVDDLNIISI 240
DB 180 TRAFMNSFTIDPKSGDLIFDPVTFAPDSGEYVCOAQNGYGTAVRSEAAHMDVAVELNVGGI 239
QY 241 IAAVVALVIVSGLGVCAQRKGYE--SKETSFOKSNSSSKATWSENDFKTKSFI 297
DB 240 VAAVLVTLILGLLIFGWFAYSRGYFETTKKGTAPGKKVIYQSPTRSEGEFKQTSSFL 299
QY 298 I 298
DB 300 V 300
RESULT 4
JAMI_BOVIN STANDARD; PRT; 298 AA.
ID JAMI_BOVIN
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AC Q9XT56;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Junctional adhesion molecule 1 precursor (JAM).
GN FLIR OR JAM1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99323940; PubMed=10395839;
RA Ozaki H., Ishii K., Horiuchi H., Arai H., Kawamoto T., Okawa K.,
RA Iwamatsu A., Kita T.;
RT "Combined treatment of TNF-alpha and IFN-gamma causes redistribution
of junctional adhesion molecule in human endothelial cells.";
RL J. Immunol. 163:553-557(1999).
CC -!- FUNCTION: Seems to plays a role in epithelial tight junction
formation. Appears early in primordial forms of cell junctions and
recruits PAR3. The association of the PAR6-PAR3 complex may
prevent the interaction of PAR3 with JAM1, thereby preventing
tight junction assembly (By similarity). Plays a role in
regulating monocyte transmigration involved in integrity of
epithelial barrier. Involved in platelet activation.
CC -!- SUBUNIT: Interacts with the first PDZ domain of PAR3. The
association between PAR3 and PAR6B probably disrupts this
interaction (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: Localized at tight junctions of both
epithelial and endothelial cells.
CC -!- SIMILARITY: Belongs to the immunoglobulin-like V-type domains.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
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CC -----
EMBL; AF111714; AAD42051.1; -.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; Igc2; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Tight junction; Immunoglobulin domain; Glycoprotein; Transmembrane;
KW Repeat; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 298 JUNCTIONAL ADHESION MOLECULE 1.
FT DOMAIN 25 237 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 238 258 POTENTIAL.
FT DOMAIN 239 298 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 28 124 IG-LIKE V-TYPE 1.
FT DOMAIN 134 227 IG-LIKE V-TYPE 2.
FT DISULFID 49 108 POTENTIAL.
FT DISULFID 152 211 POTENTIAL.
FT CARBOHYD 184 184 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 298 AA; 32456 MW; 714FE1C1714769A2 CRC64;
Query Match 27.3%; Score 415.5; DB 1; Length 298;
Best Local Similarity 35.1%; Pred. No. 7.4e-28;
Matches 107; Conservative 47; Mismatches 118; Indels 33; Gaps 10;
QY 9 LLL---LLRLVVALGYHKAYGFSAPKQDQVTVAVYQEAAILAC-----KTPKKTVXSR 60
DB 12 LLLFTSMILCSALGRGAVQY-----EPVVRVPPNNPAKLSCSYSGFSSP-----R 58
QY 61 LEWK-KLGRSVSVFYVYQOTLQGDFFKRAEMIDFNIRIKNTRSDAGKYRCEVSAPSQGQ 119


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Db 59 VEWKFTGDIRGLVYNNKITASYENRVTFTDITGTFHVSRTKDTGMVTCMVS--DEGN 116
QY 120 NLEEDVTLEVLVAPVBSCEVPSSALSGTVVVELRCODKEGPAPEYTWFKDGRILLENP 179
Db 117 TYGEVTVQLVILVPPSKPTINPVSSVTIGTRAVLTCSEKDGPPSPYKFKDGVEMPLEP 176
QY 180 RLGSQSTNSYNTMTKTLQFNTVSKLDTGEVSCFARNVSVYRCPGK---RMQVDDL 235
Db 177 KSNRAFSNNSYTLNQKTLGELIFDPVSASDTGDFTCQAN--GY-ASPVKSDTVHMDAVEL 233
QY 236 NISGITAUVVVALVSVCGLVGYCAQRKGYF--SKETSFKNSSSKATTSSENDPKHT 293
Db 234 NVGGIVAFAVFTLILGALIFGWFAISRGYDFRANKGTSNKVVIYSQPNARSDGFEFOT 293
QY 294 KSPII 298
Db 294 SSFLV 298

RESULT 5
A33 HUMAN
ID A33_HUMAN STANDARD; PRT; 319 AA.
AC Q99795;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cell surface A33 antigen precursor (Glycoprotein A33).
GN GPA33.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
TISSUE=Colon carcinoma;
RA Heath J.K., White S.J., Johnstone C.N., Catimel B., Simpson R.J.,
RA Moritz R.L., Tu G.-P., Ji H., Whitehead R.H., Groenen L.C.,
RA Scott A.M., Ritter G., Cohen L., Wolt S., Old L.J., Nice E.C.,
RA Burgess A.W.;
RA "The human A33 antigen is a transmembrane glycoprotein and a novel
RT member of the immunoglobulin superfamily.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:469-474(1997).
RN [2]
POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=97396159; PubMed=9245713;
RA Ritter G., Cohen L.S., Nice E.C., Catimel B., Burgess A.W.,
RA Moritz R.L., Ji H., Heath J.K., White S.J., Wolt S., Old L.J.,
RA Simpson R.J.;
RT "Characterization of posttranslational modifications of human A33
RT antigen, a novel palmitoylated surface glycoprotein of human
RT gastrointestinal epithelium.";
RL Biochem. Biophys. Res. Commun. 236:682-686(1997).
CC -!- FUNCTION: May play a role in cell-cell recognition and signaling.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in normal gastrointestinal
CC epithelium and in 95% of colon cancers.
CC -!- PTM: N-GLYCOSYLATED, CONTAINS APPROXIMATELY 8 KDA OF N-LINKED
CC CARBOHYDRATE.
CC -!- PTM: Palmitoylated.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC
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CC
CC EMBL; U79725; AAC50957.1; -.
CC GenBank; HGNC:4445; GPA33.
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DR MIM; 602171; -.
DR GO; GO:0005888; C:proteoglycan integral to plasma membrane; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
KW Immunoglobulin domain; Lipoprotein; Palmitate; Glycoprotein;
KW Transmembrane; Signal; Antigen.
FT SIGNAL 1 21
FT CHAIN 22 319
FT DOMAIN 22 235
FT TRANSMEN 236 256
FT DOMAIN 257 319
FT DOMAIN 22 134
FT DOMAIN 140 227
FT DOMAIN 258 261
FT DISULFID 43 117
FT DISULFID 146 222
FT DISULFID 162 211
FT CARBOHYD 112 112
FT CARBOHYD 200 200
FT CARBOHYD 223 223
SQ SEQUENCE 319 AA; 35632 MW; 9BFC7AAF45C2408E CRC64;
Query Match 15.2%; Score 231; DB 1; Length 319;
Best Local Similarity 28.6%; Pred. No. 3.1e-12;
Matches 72; Conservative 41; Mismatches 97; Indels 42; Gaps 11;
QY 30 SAPKQDVVAVYQAEILACKTPKTVXSR---LEWKKL-----GRSVSFVYQOT-LQ 80
Db 23 SVETPDVLRASQGSVTLPC-TYHTSTSSREGLIQDKLLLTHTERVVWPFSSKNVIH 81
QY 81 GD-FKRR-----AEMDFNIRIKNVTSDAGKRCFVSAPSEQQNLEEDT---VTLEV 130
Db 82 GELYKNRYSINNAEQSDASITIDLTADNGTVECSVLSMSD----LEGNTKSRVRLIV 137
QY 131 LVAPVPSCEVPSSALSQGVVELRCQDKGNPAPEYTWFKDGRILLENPRLGSQSTNSY 190
Db 138 LVPPKPECGTEGETIIGNLTQCSKEGSTPQYSWKRYNILNQEQPLAQPASGQPVSV 197
QY 191 TWNTKTLQFNTVSKLDTGEVSCFARNVSVYRCP-GKRMQVDDLNIS-----GIA 242
Db 198 LKNISTDT-----SGYICTSSNEEGTFCNITVAVRSPSMNVALYVGIAGVVA 247
QY 243 AVVVALVIVSVC 254
Db 248 ALIIIGIIYYCC 259
RESULT 6
CXAR_HUMAN STANDARD; PRT; 365 AA.
AC P78310; O00694;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Coxsackievirus and adenovirus receptor precursor (Coxsackievirus B-
DE adenovirus receptor) (hCAR) (CVB3 binding protein).
GN CXADR OR CAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=97190109; PubMed=9036860;
RA Bergelson J.M., Cunningham J.A., Brognoett G., Kurt-Jones E.,
RA Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;
RT "Isolation of a common receptor for Coxsackie B viruses and
RT adenoviruses 2 and 5.";
RT Science 275:1320-1323(1997).
```

[2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97250541; PubMed=9096337;
 RA Tomko R.P., Xu R., Philipson L.;
 RT "HCAR and MCAR: the human and mouse cellular receptors for subgroup C
 RT adenoviruses and group B coxsackieviruses";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).
 [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20008750; PubMed=10543405;
 RA Bowles K.R., Gibson J., Wu J., Shaffer L.G., Towbin J.A.,
 RA Bowles N.E.;
 RT "Genomic organization and chromosomal localization of the human
 RT coxsackievirus B-adenovirus receptor gene";
 RL Hum. Genet. 105:354-359(1999).
 [4]
 RP SEQUENCE FROM N.A.
 RX Anderson C.W., Kieleczawa J., Dunn J.J., Freimuth P.;
 RT "Sequence and expression of CXADR, the human gene for the
 RT coxsackievirus and adenovirus receptor";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 [5]
 RP SEQUENCE FROM N.A.
 RA Andersson B., Tomko R., Andersson K., Darban H., Oncu D., Mizra M.,
 RA Sollerbrant K., Sonhammer E., Philipson L.;
 RT "Putative regulatory domains in the human and mouse CAR genes";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [6]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cervix;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
 RA Villalon D.K., Wozny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: SERVES AS A RECEPTOR FOR GROUP B COXSACKIEVIRUSES AND
 CC SUBGROUP C OF ADENOVIRUSES (AD2 AND AD5).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
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 CC
 DR EMBL; Y07593; CAA68868.1; -;
 DR EMBL; U0716; AAC51234.1; -;
 DR EMBL; AF169366; AAF05908.1; -;
 DR EMBL; AF169360; AAF05908.1; JOINED.
 DR EMBL; AF169361; AAF05908.1; JOINED.
 DR EMBL; AF169362; AAF05908.1; JOINED.
 DR EMBL; AF169363; AAF05908.1; JOINED.
 DR EMBL; AF169364; AAF05908.1; JOINED.
 DR EMBL; AF169365; AAF05908.1; JOINED.

DR EMBL; AF200465; AAF24344.1; -;
 DR EMBL; AF242865; AAG01088.1; -;
 DR EMBL; AF242862; AAG01088.1; JOINED.
 DR EMBL; AF242864; AAG01088.1; JOINED.
 DR EMBL; BC003684; AAH03684.1; -;
 DR EMBL; BC010536; AAH10536.1; -;
 DR PDB; 1EAD; 13-JUL-01.
 DR PDB; 1FSW; 08-NOV-99.
 DR PDB; 1KAC; 24-NOV-99.
 DR Genew; HGNC:2559; CXADR.
 DR MIM; 602621; -;
 DR GO; GO:0005887; C-integral to plasma membrane; TAS.
 DR GO; GO:0004872; F-receptor activity; TAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_c2.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS0835; IG LIKE; 2.
 KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
 KW Repeat; 3D-structure.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 365 COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR.
 FT DOMAIN 20 237 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 238 258 POTENTIAL.
 FT DOMAIN 259 365 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 20 134 IG-LIKE C2-TYPE 1.
 FT DOMAIN 141 228 IG-LIKE C2-TYPE 2.
 FT DISULFID 41 120 BY SIMILARITY.
 FT DISULFID 162 212 BY SIMILARITY.
 FT CARBOHYD 106 106 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 201 201 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 365 AA; 40029 MW; AB01C6346CB7E64 CRC64;
 Query Match 12.9%; Score 195.5; DB 1; Length 365;
 Best Local Similarity 23.3%; Pred. No. 3.6e-09;
 Matches 67; Conservative 57; Mismatches 123; Indels 41; Gaps 9;
 QY 10 LLLLLLYVALGVHKA YGFSAPKQQVVAVVQVAILACK---TPKTVXSRLEW--- 63
 DB 3 LLLCFVLGVGVDFARSLSIITP---EEMERAKGTALVLPCKFTLSPDQGLDLEWLIS 60
 QY 64 ----KKLGRSVFVYQOTLQDF-----KNAEMIDFNIRKNTVRSAGKYR 108
 DB 61 PADNOKVDQ-VILYSGDKIYDVPDLKGRVHFTSNDLKSGDASINVTNLQSLDITGYQ 119
 QY 109 CVPASPEQGNLEBDTIVLELVNAPVSPCEVPSSALSGTVVELRCCKGNPAPEYTW 168
 DB 120 CKV----KAPGVANKKHLVVLVVPSCARCYVDGSEIGSDFKIKCEPKGSLPQIEW 175
 QY 169 FKDGIRLLENPLRGSQSTNSYTMNTKTGTLQFNTVSKLDTGEVSCSEARNVGVRRCPGK 228
 DB 176 QR-----LSDSQKMTGWLAEHTSSVSVKNASSEYSGTYSCTVVRNVGSDQCLLR 226
 QY 229 RMQVDDLAISGIIA-AVVVVALVISVCGVGYAQRKGYFSKTSFOK 275
 DB 227 LNVPPSNKAGLIAGIIGTLALALIGLIIFCCRKK---RREKYEK 271
 RESULT 7
 FAS2 DROME
 ID FAS2 DROME STANDARD; PRT; 873 AA.
 AC P34082; P34083; Q9W4M6;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE FAS2 OR EG:EG0007.3 OR CG3665.
 GN FAS2 OR EG:EG0007.3 OR CG3665.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, SUBCELLULAR LOCATION,
 RP AND TISSUE SPECIFICITY.
 RC STRAIN=Canton-S;
 RX MEDLINE=92005695; PubMed=1913818;
 RA Grunningloh G., Rehm E.J., Goodman C.S.;
 RT "Genetic analysis of growth cone guidance in Drosophila: fasciclin II
 RL functions as a neuronal recognition molecule.";
 RL Cell 67:45-57(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Gall R.F.,
 RA Sutton G.G., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.D.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Rosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalili M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lascko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pachter J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheefer F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas A., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J., Zhang K.C., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [3]
 RP REVISIONS, AND ALTERNATIVE SPLICING.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.E.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield B.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Ceisner S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RL systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [4]
 RP SEQUENCE OF 22-873 FROM N.A.
 RC STRAIN=Oregon-R;
 RX MEDLINE=20196011; PubMed=10731137;
 RA Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
 RA Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E.,
 RA Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D.,
 RA Mirana B., Karatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
 RA Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablo B.,
 RA Modolell J., Peter A., Schoettler P., Werner M., Mourikioti F.,
 RA Beinert N., Dowe G., Schaefer U., Jaekle H., Bucheton A.,
 RA Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,
 RA McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
 RA Glover D.M.;
 RT "From sequence to chromosome: the tip of the X chromosome of D.
 RL Science 287:2220-2222(2000).
 CC -!- FUNCTION: Neuronal recognition molecule for the MP1 axon pathway,
 CC pathway recognition for axons during the development of nerve
 CC fascicles.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);
 CC attached to the membrane by a GPI-anchor (isoform 2).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=3;
 CC Comment-Experimental confirmation may be lacking for some
 CC isoforms;
 CC Name=1; Synonyms=A, Membrane-linked;
 CC IsoId=P34082-1; Sequence=Displayed;
 CC Name=2; Synonyms=C, Phosphatidylinositol-linked;
 CC IsoId=P34082-2; Sequence=VSP_002508, VSP_002509;
 CC Name=3; Synonyms=B;
 CC IsoId=P34082-3; Sequence=VSP_002506, VSP_002507;
 CC -!- TISSUE SPECIFICITY: In embryos, both isoforms are initially
 CC expressed on the surface of the axons in the MP1 pathway and later
 CC on several other longitudinal axon fascicles.
 CC -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
 CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
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 CC -----
 CC EMBL; M77165; AAA28527.1; -;
 CC EMBL; M77166; AAA28528.1; -;
 CC EMBL; AL033125; CAA21825.1; -;
 CC EMBL; AE003430; AAF45925.2; -;
 CC EMBL; AE003430; AAN09119.1; -;
 CC EMBL; AL033125; CAA21826.1; -;
 CC EMBL; AL033125; CAA21826.1; -;
 CC PIR; A41054; A41054;
 CC FlyBase; FBgn000635; Fas2.
 CC GO; GO:0005886; C:plasma membrane; IDA.
 CC GO; GO:0007156; P:phospholipid cell adhesion; IDA.
 CC GO; GO:0007611; P:learning and/or memory; IMP.
 CC GO; GO:0016319; P:muscle body development; IMP.
 CC GO; GO:0008038; P:neuronal cell recognition; IDA.
 CC GO; GO:0045473; P:response to ethanol (sensu Insecta); NAS.
 CC InterPro; IPR008957; FN_III-like.
 CC InterPro; IPR003961; FN_III.
 CC InterPro; IPR007110; IG-like.
 CC Pfam; PF00041; fn3; 2.
 CC Pfam; PF00047; ig; 5.
 CC SMART; SM00060; FN3; 2.
 CC SMART; SM00408; IGC2; 3.
 CC PROSITE; PS50835; IG-LIKE; 5.
 CC Cell adhesion; Glycoprotein; Repeat; Alternative splicing;
 CC Immunoglobulin domain; Transmembrane; GPI-anchor; Signal;
 CC Neurogenesis.
 KW SIGNAL 1 28 POTENTIAL.
 KW CHAIN 29 873 FASCICLIN II.
 KW DOMAIN 29 751 EXTRACELLULAR (POTENTIAL).
 KW TRANSMEM 752 769 POTENTIAL.
 KW DOMAIN 770 769 CYTOPLASMIC (POTENTIAL).
 KW DOMAIN 31 131 IG-LIKE C2-TYPE 1.
 KW DOMAIN 138 223 IG-LIKE C2-TYPE 2.
 KW DOMAIN 230 318 IG-LIKE C2-TYPE 3.
 KW DOMAIN 323 423 IG-LIKE C2-TYPE 4.
 KW DOMAIN 428 520 IG-LIKE C2-TYPE 5.
 KW DOMAIN 544 619 FIBRONECTIN TYPE-III 1.


```
QY 188 SSVTMT-----KTGTLQNTVSKLDTGYSCARNVGVRCPCGRKMOVDDNLISGII 241
Db 180 DSQTMPTPLAETSPVSVKNASSEYSGYSCVQNRVSDQOMLRDLVPPSPNAGTI 239
QY 242 AAVVV---VALVISVCGLGVCYACR-----XGYFSKETSFQKSNM 278
Db 240 AGAVIGTLLALVIGALFCCHRRKREEKVEVHHDIREDVPPKSRSTSTARSYIGSNH 299
QY 279 SSKATTMSENDFKHTKS 295
Db 300 SSLGMSFSPNMEGYSKT 316

RESULT 9
UN89 CAEL STANDARD; PRT; 6632 AA.
AC 001761; Q17362;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Muscle M-line assembly protein unc-89 (Uncoordinated protein 89).
GN UNC-89 OR COSD1.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RC STRAIN=Bristol N2; PubMed=8603916;
EX MEDLINE=96180278;
RA Benian G.M., Tinley T.B., Tang X., Borodovsky M.;
RT "The Caenorhabditis elegans gene unc-89, required for muscle M-line
RT assembly, encodes a giant modular protein composed of Ig and signal
RT transduction domains.";
RL J. Cell Biol. 132:835-848(1996).
RN [2]
RC SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Du Z., Le T.T., Wilson R.;
RT Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RC REVISIONS.
RA Waterston R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Structural component of the muscle M-line. Myofilament
CC lattice assembly begins with positional cues laid down in the
CC basement membrane and muscle cell membrane. UNC-89 responds to
CC these signals, localizes, and then participates in assembling an
CC M-line.
CC -!- TISSUE SPECIFICITY: Localizes to the middle of A-bands.
CC -!- SIMILARITY: Contains 1 DEL-homology (DH) domain.
CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
CC -!- SIMILARITY: Contains 49 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 1 PH domain.
CC -!- SIMILARITY: Contains 5 RCSD domains.
CC -!- SIMILARITY: Contains 1 SH3 domain.
CC -----
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CC -----
CC EMBL; U30058; AAB00542.1; -
CC EMBL; AF003131; AAB54132.2; -
CC PDB; 1FHO; 20-DEC-00.
CC WormPep; C09D1.1; CB30426.
CC InterPro; IPR008957; FN.III-like.
CC InterPro; IPR003961; FN.III.
CC InterPro; IPR007110; IG-like.
```

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DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003066; IG_MHC.
DR InterPro; IPR001849; PH.
DR InterPro; IPR007850; RCSD.
DR InterPro; IPR000219; RHOGEF.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00047; IG; 47.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF05177; RCSD; 5.
DR Pfam; PF06211; RHOGEF; 1.
DR Pfam; PF00018; SH3; 1.
DR SMART; SM00408; IGC2; 23.
DR SMART; SM00325; RHOGEF; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS001010; DH_2; 1.
DR PROSITE; PS50835; IG-LIKE; 49.
DR PROSITE; PS50003; PH_DOMAIN; 1.
DR PROSITE; PS50002; SH3; 1.
KW Muscle protein; immunoglobulin domain; Repeat; SH3 domain;
KW 3D-structure.
FT DOMAIN 63 127 SH3.
FT DOMAIN 152 330 DH.
FT DOMAIN 342 438 PH.
FT DOMAIN 547 633 IG-LIKE C2-TYPE 1.
FT DOMAIN 648 736 IG-LIKE C2-TYPE 2.
FT DOMAIN 748 838 IG-LIKE C2-TYPE 3.
FT DOMAIN 946 1033 IG-LIKE C2-TYPE 4.
FT DOMAIN 1044 1132 IG-LIKE C2-TYPE 5.
FT DOMAIN 1140 1227 IG-LIKE C2-TYPE 6.
FT DOMAIN 1272 1315 THR-RICH.
FT DOMAIN 1375 1475 RCSD 1.
FT DOMAIN 1479 1585 RCSD 2.
FT DOMAIN 1597 1695 RCSD 3.
FT DOMAIN 1700 1799 RCSD 4.
FT DOMAIN 1800 1860 RCSD 5.
FT DOMAIN 1982 2067 IG-LIKE C2-TYPE 7.
FT DOMAIN 2071 2163 IG-LIKE C2-TYPE 8.
FT DOMAIN 2171 2281 IG-LIKE C2-TYPE 9.
FT DOMAIN 2269 2359 IG-LIKE C2-TYPE 10.
FT DOMAIN 2367 2455 IG-LIKE C2-TYPE 11.
FT DOMAIN 2463 2564 IG-LIKE C2-TYPE 12.
FT DOMAIN 2563 2651 IG-LIKE C2-TYPE 13.
FT DOMAIN 2657 2746 IG-LIKE C2-TYPE 14.
FT DOMAIN 2754 2858 IG-LIKE C2-TYPE 15.
FT DOMAIN 2887 2980 IG-LIKE C2-TYPE 16.
FT DOMAIN 2994 3081 IG-LIKE C2-TYPE 17.
FT DOMAIN 3087 3183 IG-LIKE C2-TYPE 18.
FT DOMAIN 3189 3280 IG-LIKE C2-TYPE 19.
FT DOMAIN 3286 3376 IG-LIKE C2-TYPE 20.
FT DOMAIN 3384 3469 IG-LIKE C2-TYPE 21.
FT DOMAIN 3482 3572 IG-LIKE C2-TYPE 22.
FT DOMAIN 3580 3667 IG-LIKE C2-TYPE 23.
FT DOMAIN 3686 3777 IG-LIKE C2-TYPE 24.
FT DOMAIN 3817 3908 IG-LIKE C2-TYPE 25.
FT DOMAIN 3920 4009 IG-LIKE C2-TYPE 26.
FT DOMAIN 4018 4106 IG-LIKE C2-TYPE 27.
FT DOMAIN 4109 4201 IG-LIKE C2-TYPE 28.
FT DOMAIN 4212 4287 IG-LIKE C2-TYPE 29.
FT DOMAIN 4302 4387 IG-LIKE C2-TYPE 30.
FT DOMAIN 4400 4485 IG-LIKE C2-TYPE 31.
FT DOMAIN 4489 4580 IG-LIKE C2-TYPE 32.
FT DOMAIN 4588 4678 IG-LIKE C2-TYPE 33.
FT DOMAIN 4681 4771 IG-LIKE C2-TYPE 34.
FT DOMAIN 4873 4961 IG-LIKE C2-TYPE 35.
FT DOMAIN 4965 5057 IG-LIKE C2-TYPE 36.
FT DOMAIN 5067 5160 IG-LIKE C2-TYPE 37.
FT DOMAIN 5171 5260 IG-LIKE C2-TYPE 38.
FT DOMAIN 5277 5366 IG-LIKE C2-TYPE 39.
FT DOMAIN 5383 5472 IG-LIKE C2-TYPE 40.
FT DOMAIN 5487 5578 IG-LIKE C2-TYPE 41.
FT DOMAIN 5595 5685 IG-LIKE C2-TYPE 42.
FT DOMAIN 5701 5790 IG-LIKE C2-TYPE 43.
```


DR PROSITE, PS00240; RECEPTOR TYR KIN III; 1.
KW Angiogenesis; Signal, Transferase; Tyrosine-protein kinase; Receptor;
KW Transmembrane; Glycoprotein; Phosphorylation; ATP-binding;
KW Immunoglobulin domain; Repeat
FT SIGNAL 1 19
FT CHAIN 20 1367
FT
FT DOMAIN 20 762
FT TRANSMEM 763 784
FT DOMAIN 785 1367
FT
FT DOMAIN 46 111
FT DOMAIN 143 209
FT DOMAIN 226 325
FT DOMAIN 330 416
FT DOMAIN 423 542
FT DOMAIN 549 656
FT DOMAIN 665 751
FT DOMAIN 832 1160
FT NP_BIND 838 846
FT BINDING 866 866
FT ACT_SITE 1026 1026
FT CARBOHYD 46 46
FT CARBOHYD 98 98
FT CARBOHYD 145 145
FT CARBOHYD 160 160
FT CARBOHYD 247 247
FT CARBOHYD 320 320
FT CARBOHYD 376 376
FT CARBOHYD 397 397
FT CARBOHYD 509 509
FT CARBOHYD 521 521
FT CARBOHYD 578 578
FT CARBOHYD 611 611
FT CARBOHYD 617 617
FT CARBOHYD 629 629
FT CARBOHYD 673 673
FT CARBOHYD 702 702
FT CARBOHYD 719 719
FT MOD_RES 1057 1057
FT CONFLICT 25 25
FT CONFLICT 679 679
FT CONFLICT 783 784
FT CONFLICT 917 917
FT CONFLICT 1341 1367
SQ SEQUENCE 1367 AA; 152516 MW; EFC99704FIDCA266 CRC64;
Query Match 10.6%; Score 160.5; DB 1; Length 1367;
Best Local Similarity 24.8%; Pred. No. 1.7e-05;
Matches 53; Conservative 23; Mismatches 75; Indels 63; Gaps 6;
QY 44 QEAILACKTPKTKVSKLEWKKGRSVFVYQOTLOGDFKNRAEMIDFN----- 93
Db 562 QESVSLCTADNTFENLTWYKLSQATSVHGESLTPVCKNLDALWKLNGTFPSNSTND 621
QY 94 ---IRKNVTRSDAGKYRC-----EVSAPSEQONLEEDTVTLEV 130
Db 622 ILIVAFQNASIQDQDVYCSAQDKTKRKHCLVQLIILERMAMPITG-NLENQT-TI-- 678
QY 131 LVAFAVPSCEVPSSALSTVVELRCQKGNPAPEYTFWKGITLLENPLRGQSINSSY 190
Db 679 -----GETIEVTC-PASGNPTPHITWFKDNETLVDSGIVLRDGNRL 720
QY 191 TMTNKTGTLQNTVSKLDTGYSCEARNSVGYYR 224
Db 721 TI-----RRVRKEDGGYLTQACNVLCAR 745
RESULT 12
NCM2 MOUSE
ID NCM2_MOUSE STANDARD; PRT; 837 AA.
AC O35136; O35962;
DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neural cell adhesion molecule 2 precursor (N-CAM 2) (RB-8 neural cell
DE adhesion molecule) (R4B12).
GN NCAM2 OR OCAM OR RNCAM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RC STRAIN=BALB/c; TISSUE=Olfactory neuroepithelium;
RX MEDLINE=97368238; PubMed=9221781;
RA Yoshihara Y., Kawasaki M., Tamada A., Fujita H., Hayashi H.,
RA Kagamiyama H., Mori K.;
RT "OCAM: A new member of the neural cell adhesion molecule family
RT related to zone-to-zone projection of olfactory and vomeronasal
RT axons".
RL J. Neurosci. 17:5830-5842(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RC STRAIN=C57BL/6J; TISSUE=Olfactory epithelium;
RX MEDLINE=97476194; PubMed=9334170;
RA Alenius M., Bohm S.;
RT "Identification of a novel neural cell adhesion molecule-related gene
RT with a potential role in selective axonal projection".
RL J. Biol. Chem. 272:26083-26086(1997).
CC -!- FUNCTION: May play important roles in selective fasciculation and
CC zone-to-zone projection of the primary olfactory axons.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (long isoform) and
CC attached to the membrane by a GPI-anchor (short isoform).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoID=O35136-1; Sequence=Displayed;
CC Name=Short;
CC IsoID=O35136-2; Sequence=VSP_002590;
CC -!- TISSUE SPECIFICITY: Expressed in subsets of both olfactory and
CC vomeronasal neurons in a zone-specific manner.
CC -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
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DR EMBL; AF001287; AAB69125.1; -
DR EMBL; AF001286; AAB69124.1; -
DR EMBL; AF016619; AAC53375.1; -
DR MGD; MGI:97282; Ncam2.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; ig; 5.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00408; IGC2; 5.
DR PROSITE; PS50835; IG_LIKE; 5.
KW Cell adhesion; Transmembrane; Glycoprotein; Repeat;
KW Immunoglobulin domain; Signal; GPI-anchor; Alternative splicing.
FT SIGNAL 1 19
FT CHAIN 20 837
FT DOMAIN 20 897
FT TRANSMEM 698 718
FT DOMAIN 719 837
FT DOMAIN 21 108
FT DOMAIN 113 202
FT DOMAIN 208 297


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DR InterPro: IPR002154; Neuregulin.
DR Pfam: PF00008; EGF; 1.
DR Pfam: PF00047; 1g; 1.
DR Pfam: PF02158; Neuregulin; 1.
DR SMART: SM00181; EGF; 1.
DR SMART: SM00408; IGG2; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS00026; EGF_3; 1.
DR PROSITE: PS00835; IG-LIKE; 1.
DR PROSITE: PS0835; IG-LIKE; 1.
DR Growth factor; EGF-like domain; Immunoglobulin domain; Glycoprotein;
KW Transmembrane; Multigene family; Alternative splicing.
KW PROPEP 1
FT CHAIN 128 868 PRO-NEUREGULIN-2, MEMBRANE-BOUND FORM.
FT CHAIN 128 868 NEUREGULIN-2
FT CHAIN 128 428 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 128 429 INTERNAL SIGNAL SEQUENCE (POTENTIAL).
FT TRANSMEM 430 450 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 451 868 IG-LIKE C2-TYPE.
FT DOMAIN 253 348 SER/THR-RICH.
FT DOMAIN 346 356 EGF-LIKE.
FT DOMAIN 357 398 POLY-SER.
FT DOMAIN 22 32 POLY-SER.
FT DOMAIN 35 45 POLY-SER.
FT DOMAIN 56 59 POLY-THR.
FT DOMAIN 103 106 POLY-ALA.
FT DOMAIN 739 745 POLY-PRO.
FT DISULFID 273 327 BY SIMILARITY.
FT DISULFID 361 375 BY SIMILARITY.
FT DISULFID 369 386 BY SIMILARITY.
FT DISULFID 388 397 BY SIMILARITY.
FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 362 362 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 1 108 Missing (in isoform 7).
FT VARSPLIC 220 222 PLV -> FFF (in isoform 3).
FT VARSPLIC 388 388 /FTID=VSP_003466.
FT VARSPLIC 389 868 Missing (in isoform 5).
FT VARSPLIC 390 412 Missing (in isoform 7).
FT VARSPLIC 390 421 NGFGQRCLEKRLRLYMPDPKQHLGFELKE -> VGYTGDRCOQFAMV
FT VARSPLIC 414 421 Missing (in isoform 2 and isoform 3).
FT VARSPLIC 414 439 HLGELKEBELYKRVITITGICVA -> SVLWDTFGTV
FT VARSPLIC 440 868 Missing (in isoform 6).
FT CONFLICT 117 117 S -> F (IN REF. 2).
FT CONFLICT 724 724 R -> H (IN REF. 2).
SQ SEQUENCE 868 AA; 93776 MW; 3C7D4D94DBE64DE2 CRC64;

Query Match
Best Local Similarity 20.3%; Score 157; DB 1; Length 868;
Matches 56; Conservative 24; Mismatches 86; Indels 36; Gaps 8;

Qy 66 LCRSVFVYQOTLQGB--FKVAREMTDFNIRKNVTRSDAGYKRCVSPSQGNLEE 123
Db 204 LERNQRVFFLEPEQPLVFTKTAAPDPN--GKNI--KKEVGKILCTDCATRPKLKKMS 260
Qy 124 DTVTLELVAPVSPCEVPSSALSGTVVLRCDKGNPAPETWFKDGRIRLENPLGS 183
Db 261 QTGEV-----GEKQSLKCEAAAGNQPQSYRWPKDGKELNR-----S 296
Qy 184 QSTNSSTYMTNKTGTLOFNVSKLDTGEYCEARNVGVRCRCRGMQVDDINI-----S 238
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Db 297 RDIRIKNGRKNRSLQFNKVKVEDAGEYVCEAENILGKDTVRG-RLHVSNSVTLLSSWS 355
Qy 239 GIIAAVVVVVALVIVSVCGLGVCY 260
Db 356 GHARKCNETAKSYCVNG-GVCY 376

RESULT 14
NRG2_MOUSE
ID NRG2_MOUSE STANDARD; PRT; 756 AA.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Pro-neuregulin-2 precursor (Pro-NRG2) [Contains: Neuregulin-2 (NRG-2)
DE (Divergent of neuregulin 1) (DON-1)].
GN NRG2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A. (ISOFORMS NRG2-5; NRG2-10 AND NRG2-16A).
RX STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=97311398; PubMed=9168115;
RA Carraway K.L. III, Weber J.L., Unger M.J., Ledesma J., Yu N.,
RA Gassmann M., Lai C.;
RT "Neuregulin-2, a new ligand of ErbB3/ErbB4-receptor tyrosine
RT kinases.";
RL Nature 387:512-516 (1997).
RN [2]
RP SEQUENCE OF 150-756 FROM N.A. (ISOFORMS DON-1M AND DON-1S).
RC TISSUE=Choroid plexus;
RX MEDLINE=97342638; PubMed=9199335;
RA Busfield S.J., Michnick D.A., Chickering T.W., Revett T.L., Ma J.,
RA Woolf E.A., Comrack C.A., Dussault B.J., Woolf J., Goodearl A.D.J.,
RA Gearing D.P.;
RT "Characterization of a neuregulin-related gene, Don-1, that is highly
RT expressed in restricted regions of the cerebellum and hippocampus.";
RL Mol. Cell. Biol. 17:4007-4014 (1997).
CC -!- FUNCTION: Direct ligand for ERBB3 and ERBB4 tyrosine kinase
CC receptors. Concomitantly recruits ERBB1 and ERBB2 coreceptors,
CC resulting in ligand-stimulated tyrosine phosphorylation and
CC activation of the ERBB receptors. May also promote the
CC heterodimerization with the EGF receptor.
CC -!- SUBCELLULAR LOCATION: EXISTS AS AN TYPE I MEMBRANE PROTEIN AND AS
CC A PROTEOLYTICALLY RELEASED SOLUBLE GROWTH FACTOR FORM. THE
CC MEMBRANE-BOUND FORM DOES NOT SEEM TO BE ACTIVE (BY SIMILARITY).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Comment=Additional isoforms seem to exist;
CC Name=NRG2-16A;
CC IsoId=P56974-1; Sequence=Displayed;
CC Name=DON-1M;
CC IsoId=P56974-2; Sequence=VSP_003464;
CC Name=DON-1S; Synonyms=NRG2-5;
CC IsoId=P56974-3; Sequence=VSP_003462; VSP_003463;
CC Name=NRG2-10;
CC IsoId=P56974-4; Sequence=VSP_003460; VSP_003461;
CC -!- TISSUE SPECIFICITY: Highest expression in the brain, with lower
CC levels in the lung. In the cerebellum, found in granule and
CC Purkinje cells.
CC -!- DOMAIN: The cytoplasmic domain may be involved in the regulation
CC of trafficking and proteolytic processing. Regulation of the
CC proteolytic processing involves initial intracellular domain
CC dimerization (By similarity).
CC -!- DOMAIN: ERBB receptor binding is elicited entirely by the EGF-like
CC domain (By similarity).
CC -!- PTM: Proteolytic cleavage close to the plasma membrane on the
CC external face leads to the release of the soluble growth factor
CC form (By similarity).
CC -!- PTM: Extensive glycosylation precedes the proteolytic cleavage (By
```


DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00041; fn3; 7.
DR Pfam; PF00047; ig; 3.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00014; FNTYPEIII.
DR PRINTS; PR00700; FNTYPEPHASE.
DR SMART; SM00060; FN3; 4.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00383; TYR_PHOSPHATASE 1; 2.
DR PROSITE; PS0056; TYR_PHOSPHATASE 2; 2.
DR PROSITE; PS0055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;
KW Cell adhesion; Immunoglobulin domain; Repeat; 3D-structure.
FT SIGNAL 1 16
FT CHAIN 17 1897
FT DOMAIN 17 1897 LAR PROTEIN.
FT DOMAIN 17 1250 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1251 1274 POTENTIAL.
FT DOMAIN 1275 1897 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 23 113 IG-LIKE C2-TYPE 1.
FT DOMAIN 125 214 IG-LIKE C2-TYPE 2.
FT DOMAIN 222 304 IG-LIKE C2-TYPE 3.
FT DOMAIN 1360 1606 PROTEIN-TYROSINE PHOSPHATASE 1.
FT DOMAIN 1649 1897 PROTEIN-TYROSINE PHOSPHATASE 2.
FT ACT_SITE 1538 1538 PHOSPHOCYSTEINE INTERMEDIATE (BY
SIMILARITY).
FT ACT_SITE 1829 1829 PHOSPHOCYSTEINE INTERMEDIATE (BY
SIMILARITY).
FT CARBOHYD 107 107 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 240 240 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 711 711 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 956 956 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MUTAGEN 1538 1538 C->S; LOSS OF ACTIVITY.
SQ SEQUENCE 1897 AA; 211844 MW; 439950FID5C031FF CRC64;
Query Match 10.3%; Score 156; DB 1; Length 1897;
Best Local Similarity 25.8%; Pred.No. 6e-05;
Matches 59; Conservative 35; Mismatches 89; Indels 46; Gaps 10;
QY 11 LLLLYLVVALGYHKAYGFSAPKQQVVTAVYQCEAILACKT---PKTKVKSRLWKKLK 67
DB 8 LVMLGLVAGAGDGRKVPFIKVPEDQ---TGLSGGVASFVCOATGEPK----PRITWKKG 60
QY 68 RSVSFVYYQQTLOGDFKNRAEMIDFN-----IRKNV-TRSDAGKYRCEVSAPSEQQN 120
DB 61 KKVS-----SQRFVIEFDGAGSVLRIQPLRVQRDEAIVECTATNSLGEINT 108
QY 121 LEEDTVTLVLVAVPSC-----VPSSALSGTVVELRCODKEGNPAPEYTWFKDGIR 174
DB 109 SAKLSVLEEELPPGFPIDNGPOLKVVERKARTATML---CA-AGGNPDPEISWFKDPLP 164
QY 175 LLENPRLGQSTNSYTMNTKTGTQLQNTVSKLDTGYSCEARNSVGVR 223
DB 165 V-----DPATSNGRIRQLRSGALQIESSEESDQKGYECVATNSAGTR 206

Search completed: July 15, 2004, 23:53:11
Job time : 13.7487 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2004, 23:49:33 ; Search time 52.5882 Seconds

(without alignments)
1787.936 Million cell updates/sec

Title: US-09-852-797-76

Perfect score: 1521

Sequence: 1 MARRSRRLRLRLRLVLA.....SSKATTSENDPFGHTKSFII 298

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 segs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 25:**

1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mbc:
8: sp_organelle:
9: sp_phase:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_virus:
16: sp_bacteriaph:
17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1215	79.9	298	11	Q9JI59 mus musculus
2	1212	79.7	298	11	Q8CE95 mus musculus
3	1212	79.7	298	11	Q8CE95 mus musculus
4	507.5	33.4	181	11	Q9CWD9 mus musculus
5	499	32.8	310	11	Q9D8B7 mus musculus
6	499	32.8	310	11	Q9EPK4 mus musculus
7	495	32.6	310	11	Q9D1M9 mus musculus
8	481	31.6	310	4	Q9BX67 mus musculus
9	481	31.6	355	4	Q8WML8 mus musculus
10	480	31.6	309	4	Q96FL1 mus musculus
11	453	29.8	300	13	Q7SYQ7 xenopus lae
12	435	28.6	289	13	Q7ZWT0 xenopus lae
13	421	27.7	300	11	Q8VC39 mus musculus
14	409.5	26.9	300	11	Q9JHY1 mus musculus
15	393.5	25.9	299	4	Q9YB22 mus musculus
16	315.5	20.7	173	11	Q9JKD5 mus musculus

17	227	14.9	318	13	Q91664 xenopus lae
18	225	14.8	335	13	Q9PW4 gallus gall
19	224	14.7	335	13	Q9YGH1 gallus gall
20	221	14.5	319	11	Q922D5 mus musculus
21	219	14.4	319	11	Q9JKA5 mus musculus
22	219	14.4	335	13	Q9YGV5 gallus gall
23	217	14.3	181	13	Q91665 xenopus lae
24	210	13.8	259	4	Q7Z2Q1 homo sapien
25	210	13.8	387	4	Q8EXK7 homo sapien
26	205.5	13.5	319	6	Q9TU80 canis famli
27	202	13.3	390	4	Q96T50 homo sapien
28	202	13.3	390	4	Q96AP7 homo sapien
29	201.5	13.2	365	6	Q8WV3 bos taurus
30	201.5	13.2	394	11	Q925E2 mus musculus
31	197	13.0	407	11	Q9D2J4 mus musculus
32	195.5	12.9	344	4	Q8UKV4 homo sapien
33	195	12.8	390	6	Q95KI3 macaca fasc
34	194	12.8	298	13	Q804R4 brachydanio
35	194	12.8	372	13	Q90Y50 mus musculus
36	191	12.6	319	6	Q8TU79 sus scrofa
37	188	12.4	430	4	Q8N4F1 homo sapien
38	186	12.2	773	5	Q8IRS5 drosophila
39	183	12.0	300	11	Q9DA22 mus musculus
40	183	12.0	300	11	Q9D9J0 mus musculus
41	180	11.8	352	11	Q91W66 mus musculus
42	180	11.8	365	11	Q9DBJ8 mus musculus
43	179.5	11.8	304	11	Q9CVA4 mus musculus
44	179.5	11.8	323	4	Q8NDD2 homo sapien
45	177	11.6	284	4	Q9NX42 homo sapien

ALIGNMENTS

RESULT 1

ID	Q9JI59	PRELIMINARY;	PRT;	298	AA.
AC	Q9JI59;				
DT	01-OCT-2000	(TREMELrel. 15, Created)			
DT	01-OCT-2000	(TREMELrel. 15, Last sequence update)			
DT	01-OCT-2003	(TREMELrel. 25, Last annotation update)			
DE	Vascular endothelial junction-associated molecule (Junctional adhesion molecule-3) (2410030G21Rik protein).				
DE	JAM2 OR JCAM3 OR JCAM2 OR JAM-3 OR 2410030G21RIK.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1] SEQUENCE FROM N.A.				
RP	STRAIN=CS7BL/6J;				
RC	MEDLINE=20317114; PubMed=10779521;				
RX	Palmeri D., van Zante A., Huang C.-C., Hemmerich S., Rosen S.D.;				
RA	"Vascular Endothelial Junction-associated Molecule, a Novel Member of the Immunoglobulin Superfamily, is Localized to Intercellular Boundaries of Endothelial Cells."				
RT	J. Biol. Chem. 275:19139-19145(2000).				
RL	[2] SEQUENCE FROM N.A.				
RN	STRAIN=CS7BL/6J; PubMed=11036763;				
RP	Aurand-Lions M.A., Durcan L., Du Pasquier L., Imhof B.A.;				
RX	"Cloning of JAM-2 and JAM-3: an Emerging Junctional Adhesion Molecular Family?"				
RT	Curr. Top. Microbiol. Immunol. 251:91-98(2000).				
RL	[3] SEQUENCE FROM N.A.				
RN	STRAIN=CS7BL/6J; Tissue=Embryo, and Embryonic stem cells;				
RP	MEDLINE=21085560; PubMed=11217851;				
RX	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,				
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,				
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,				
RA	Saio T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saio R.,				
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,				

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaio I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniwa M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyszaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AF255911; AAF81224.1; -
DR EMBL; AJ291757; BAC20699.1; -
DR EMBL; AK013914; BAC29053.1; -
DR EMBL; AK010616; BAB27064.1; -
DR MGD; MGI:1933820; Jam2.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 2.
DR PROSITE; PS50835; IG LIKE; 2.
SQ SEQUENCE 298 AA; 33047 MW; 1124E0F07E6CF751 CRC64;

Query Match 79.9%; Score 1215; DB 11; Length 298;
Best Local Similarity 78.6%; Pred. No. 9.5e-106;
Matches 235; Conservative 25; Mismatches 37; Indels 2; Gaps 2;

QY 1 MARRSRHRLLLRLYLVALGYHAYGFSAPKD-QQVTVAVXYQAEAILACKTPKKTVS 59
Db 1 MARSPOGLMLLLHLYLVALDYHANGFSASKDHROEVTVIEFQAEAILACKTPKKTSS 60

QY 60 RLEWKLGRSVSFVYQOTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG 119
Db 61 RLEWKKVGGVSLVYQQALQGFDFKRAEMIDFNIRIKNVTRSDAGEYRCEVSAPTEQ 120

QY 120 NLEEDTVLEVLVAPVSPCEVPSSALSGTVVLELRCQDKEGNPAPEYTWFKDGIIRLENP 179
Db 121 NLQEDKVMLEVLVAPVAPACEVPTSVMTGVSVELRCQDKEGNPAPEYTWFKDGTSLGNP 180

QY 180 RLGSOSTSSYTMNTKTGTLQFNVTSCLDTEYSCAARNVGYRCPGKRMQVDDNLISG 239
Db 181 K-GGTHNNSYTMNTKSGILQFNMISKWDSGEYCEARNVGHRRCPGKRMQVDVNLISG 239

QY 240 IIAAVVVALVSVCGLGVCYQAQRGYFSKETSFKQSNSSKATMTSENDFKHTKSFII 298
Db 240 IIAATVVAVVISVCGLGTCYQAQRGYFSKETSFKQSPASKVTMTSENDFKHTKSFII 298

RESULT 2
Q8CE95 PRELIMINARY; PRT; 298 AA.
ID Q8CE95;
AC Q8CE95;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Junction cell adhesion molecule 2.
GN JAM2 OR JCAM2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RL EMBL; AK078128; BAC37139.1; -
DR MGD; MGI:1933820; Jam2.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
SQ SEQUENCE 298 AA; 33182 MW; 1131F0BFD89CEB51 CRC64;

Query Match 79.7%; Score 1212; DB 11; Length 298;
Best Local Similarity 78.3%; Pred. No. 1.8e-105;
Matches 234; Conservative 26; Mismatches 37; Indels 2; Gaps 2;

QY 1 MARRSRHRLLLRLYLVALGYHAYGFSAPKD-QQVTVAVXYQAEAILACKTPKKTVS 59
Db 1 MARSPOGLMLLLHLYLVALDYHANGFSASKDHROEVTVIEFQAEAILACKTPKKTSS 60

QY 60 RLEWKLGRSVSFVYQOTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQG 119
Db 61 RLEWKKVGGVSLVYQQALQGFDFKRAEMIDFNIRIKNVTRSDAGEYRCEVSAPTEQ 120

QY 120 NLEEDTVLEVLVAPVSPCEVPSSALSGTVVLELRCQDKEGNPAPEYTWFKDGIIRLENP 179
Db 121 NLQEDKVMLEVLVAPVAPACEVPTSVMTGVSVELRCQDKEGNPAPEYTWFKDGTSLGNP 180

QY 180 RLGSOSTSSYTMNTKTGTLQFNVTSCLDTEYSCAARNVGYRCPGKRMQVDDNLISG 239
Db 181 K-GGTHNNSYTMNTKSGILQFNMISKWDSGEYCEARNVGHRRCPGKRMQVDVNLISG 239

QY 240 IIAAVVVALVSVCGLGVCYQAQRGYFSKETSFKQSNSSKATMTSENDFKHTKSFII 298
Db 240 IIAATVVAVVISVCGLGTCYQAQRGYFSKETSFKQSPASKVTMTSENDFKHTKSFII 298

RESULT 3
Q8CE95 PRELIMINARY; PRT; 298 AA.
ID Q8CE95;
AC Q8CE95;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Junction cell adhesion molecule 2.
GN JAM2 OR JCAM2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RL EMBL; AK078128; BAC37139.1; -
DR MGD; MGI:1933820; Jam2.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
SQ SEQUENCE 298 AA; 33182 MW; 1131F0BFD89CEB51 CRC64;

Query Match 79.7%; Score 1212; DB 11; Length 298;

```
Best Local Similarity 78.6%; Pred. No. 1.8e-105;
Matches 235; Conservative 25; Mismatches 37; Indels 2; Gaps 2;

QY 1 MARRSRHELLLLRLVYLVAGYHKGAFSPKD-QQVTVAVYQEAALACKTPKTKVXS 59
Db 1 MARSQGLMLLLHLHYLVYLVAGYHKGAFSPKD-QQVTVAVYQEAALACKTPKTKVXS 60
QY 60 RLEWKKLGRSVFVYVYQQTQGGDFKNRAEMIDFNIRIKNVTSDAGKYRCEVSAPSEQG 119
Db 61 RLEWKKVGGVSLVYVYQQAQGGDFKNRAEMIDFNIRIKNVTSDAGKYRCEVSAPSEQG 120
QY 120 NLEEDTVTLVLEVL 131
Db 121 NLQEDKVMLEVL 132

RESULT 4
Q9CWD9 PRELIMINARY; PRT; 181 AA.
ID Q9CWD9 Q9D8B7 Q9D8B7 PRELIMINARY; PRT; 310 AA.
AC Q9D8B7 Q9D8B7 PRELIMINARY; PRT; 310 AA.
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 2410167M24Rik protein (Junction cell adhesion molecule 2).
GN JAM2 OR JCAM2 OR 2410167M24Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryonic stem cells;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL ENBL; AK010826; BAB27208.1; -.
DR ENBL; AK045095; BAC32219.1; -.
DR MGD; MGI:1933820; Jam2.
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DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
SQ SEQUENCE 181 AA; 20330 MW; 603B6114FBB11AEB CRC64;

Query Match 33.4%; Score 507.5; DB 11; Length 181;
Best Local Similarity 76.5%; Pred. No. 1.5e-39;
Matches 101; Conservative 12; Mismatches 18; Indels 1; Gaps 1;

QY 1 MARRSRHELLLLRLVYLVAGYHKGAFSPAKO-QQVTVAVYQEAALACKTPKTKVXS 59
Db 1 MARSQGLMLLLHLHYLVYLVAGYHKGAFSPAKO-QQVTVAVYQEAALACKTPKTKVXS 60
QY 60 RLEWKKLGRSVFVYVYQQTQGGDFKNRAEMIDFNIRIKNVTSDAGKYRCEVSAPSEQG 119
Db 61 RLEWKKVGGVSLVYVYQQAQGGDFKNRAEMIDFNIRIKNVTSDAGKYRCEVSAPSEQG 120
QY 120 NLEEDTVTLVLEVL 131
Db 121 NLQEDKVMLEVL 132

RESULT 5
Q9D8B7 PRELIMINARY; PRT; 310 AA.
ID Q9D8B7 Q9D8B7 PRELIMINARY; PRT; 310 AA.
AC Q9D8B7 Q9D8B7 PRELIMINARY; PRT; 310 AA.
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 1110002N23Rik protein.
GN JCAM3 OR JCAM2 OR 1110002N23Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL ENBL; AK010826; BAB27208.1; -.
DR ENBL; AK045095; BAC32219.1; -.
DR MGD; MGI:1933820; Jam2.
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RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauble F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Cariboidi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kotsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK003326; BAB22715.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Immunoglobulin domain.
SQ SEQUENCE 310 AA; 34819 MW; 6692BCAD68EA81D CRC64;

Query Match 32.6%; Score 496; DB 11; Length 310;
Best Local Similarity 37.0%; Pred. No. 3.7e-38;
Matches 117; Conservative 61; Mismatches 112; Indels 26; Gaps 9;

QY 1 MARRSRHRL-----LILLRLVLYVALGYHKAYGFSAPKQDVVTVXVYQEAAILAC-K 51
DB 3 LSRRRLRLVRLVLPDFLLLLFRGCMV-----EAVNLKSNRPVPH--EFESVELSCII 55
QY 52 TPKRTVKSRLWKKL-GRSVFVYVYQTLQGDFFKNRAEMI-DPNIRIKNVTRSDAGKYRC 109
DB 56 TDSQTSDPRIEKKIQDQQTIVYVFNKIQGLDLAGRTDVFGLKSLRIWVTRSDAISYRC 115
QY 110 EVSAPSEQQNLEEDVTLEVLVAPVAPVPSCEVPSSALSGLTVVLRCDKEGNPAPETWF 169
DB 116 EVVALNDR-KEVDEITIELTVQVKPVTFCVRIFAAVPVGKTATLQCCSEGGYPRPHYSW 174
QY 170 KDGIRLLENPRLGQSNTSSYTNMTKTGTITQFNTVSKLDTGEYSCEARNVSVYRCPGKR 229
DB 175 RNDVPLPTDSRANPRFNSFFHVNSEITGLVFNVAHVHKDDSGQYVCIASNDAGAARCEGD 234
QY 230 MQVDDNLNIGIIAAVVVVALVIVSVCGLGVCYAKRGYF--SKE-----TSFQKSNSSKA 282
DB 235 MEVVDNLNIGIIGVVLVILVLAITMGICAYRRGCFISSKQDGESYKSPGRHGDGVNYI 294
QY 283 TTMSNDFKHTKSFII 298
DB 295 RTSEEGDFKHIAFVI 310

RESULT 8
Q9BX67 PRELIMINARY; PRT; 310 AA.
AC Q9BX67; 2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
DE Junctional adhesion molecule 3 precursor (Junctional adhesion
DE molecule-2) (Junctional adhesion molecule-3) (Hypothetical protein
DE FLJ90288) (Hypothetical protein FLJ90828).
GN JAM-2 OR JAM3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
EN [1]
RN SEQUENCE FROM N.A.
RC Tissue=Brain;

```

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RA Cunningham S.A., Arrate M.P., Tran T.M.;
RT "Cloning of Human Junctional Adhesion Molecule 3.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RA Aurand-Lions M.A., Johnson-leger C., Wong C., Dupasquier L.;
RT "Heterogeneity of endothelial junctions is reflected by differential
RT expression and specific subcellular localization of the three JAM
RT family members.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RA Aurand-Lions M.A., Johnson-leger C., Lamagna C., Ozaki H., Kita T.;
RT "Junctional adhesion molecules (JAMs) and interendothelial
RT junctions.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
[4]
RN SEQUENCE FROM N.A.
RA Sachs U.J.H., Eva O., Berghoefer H., Santoso S.;
RT "Characterization of Junctional Adhesion Molecule-3 on Human
RT Platelets: A New Member of Immunoglobulin Superfamily.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
[5]
RN SEQUENCE FROM N.A.
RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RT "NED0 human cDNA sequencing project.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF356518; AAK27221.1; -.
DR EMBL; AJ344431; CAC69845.1; -.
DR EMBL; AF448478; AAM20925.1; -.
DR EMBL; AK074769; BAC11195.1; -.
DR EMBL; AK075309; BAC11536.1; -.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Hypothetical protein; Signal.
FT SIGNAL 1 30 POTENTIAL.
SQ SEQUENCE 310 AA; 35020 MW; CE39ADF33EADAB9 CRC64;

Query Match 31.6%; Score 481; DB 4; Length 310;
Best Local Similarity 35.8%; Pred. No. 9.6e-37;
Matches 114; Conservative 60; Mismatches 116; Indels 28; Gaps 10;

QY 1 MARRSRHRL-----LILLRLVLYVALGYHKAYGFSAPKQDVVTVXVYQEAAILAC 50
DB 1 MARRSRHRLCARLPDFLLFRGLIG-----AVNLKSNRPVQV--EFESVELSC 53
QY 51 -KTPKRTVKSRLWKKL-GRSVFVYVYQTLQGDFFKNRAEMI-DPNIRIKNVTRSDAGKY 107
DB 54 IITDSQTSDPRIEKKIQDQQTIVYVFNKIQGLDLAGRAEILGKTSKINWVTRSDALY 113
QY 108 RCEVAPSEQQNLEEDVTLEVLVAPVAPVPSCEVPSSALSGLTVVLRCDKEGNPAPETW 167
DB 114 RCEVARNDR-KEIDEIVIELTVQVKPVTFCVRIFAAVPVGKTATLQCCSEGGYPRPHYS 172
QY 168 WFKDGIRLLENPRLGQSNTSSYTNMTKTGTITQFNTVSKLDTGEYSCEARNVSVYRCPG 227
DB 173 WYNDVPLPTDSRANPRFNSFFHVNSEITGLVFNVAHVHKDDSGQYVCIASNDAGAARCE 232
QY 228 KMQVDDNLNIGIIAAVVVVALVIVSVCGLGVCYAKRGYF--SKE--TSFQ---KSNSSS 280
DB 233 QEMEVVDNLNIGIIGVVLVILVLAITMGICAYRRGCFISSKQDGESYKSPGRHGDGVN 292
QY 281 KATTMSNDFKHTKSFII 298
DB 293 YIRTDEEGDFKHKSFVI 310

RESULT 9

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RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshnyuk S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeslee R.W., Touchman J.W., Green E.B., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smallos D.E., Schmerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RT	[3]
RN	SEQUENCE FROM N.A.
RP	TISSUE=Whole;
RC	Klein S., Strausberg R.; Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RA	EMBL; BC054305; AAH54305.1; -
DR	Hypothetical protein.
RL	NON_TER ¹
XW	FT SEQUENCE 300 AA; 32858 MW; 02BC49DC74E27D14 CRC64;
SQ	Query Match 29.8%; Score 453; DB 13; Length 300; Best Local Similarity 35.5%; Pred. No. 3.9e-34; Matches 98; Conservative 59; Mismatches 101; Indels 18; Gaps 6;
QY	28 GFSAKPDQOVTVAVYQBAILACTPKTKVXRLEWKGLGR--SVSFVYYQTLOGDPKN 85 : : : : : : : : : : : : : : :
Db	38 GVTAPE-DPTITVKEGSDFLRCSYTDYNPRVEKFVNKDQETSFVDGSLTASYKD 95 : : : : : : : : : : : : : : :
QY	85 RAEMIDFNIRIKNVTRSDAGKYRCCEVSAPSEQ---GNILEEDVTTLVLVAVPVSECPV 142 : : : : : : : : : : : : : : :
Db	96 RATSPYOGIKLVNQVRKDAQGYSECVSTGTKVLYG----EAQLQIVAFCTPAQVP 151 : : : : : : : : : : : : : : :
QY	143 SSALSGTGVVELRCODKEGNPAPEYTFXKGRIILLENPRLGSQTSNGSYNTKTGTLOPN 202 : : : : : : : : : : : : : : :
Db	152 SSARTGSVAELMCMVETQGFPPLPTFTWHNN-----NSPMQAQSQNSTYTIDPNTGVLKFA 205 : : : : : : : : : : : : : : :
QY	203 TVSKLDLTGEYSCEARNISVGRRCPCKMQVDNLNISGHIAA VVVVALVISGVLGVCVAAQ 262 : : : : : : : : : : : : : : :
Db	206 SVGTSDSGBIYCANKANSQGESSAIVRMVMKDVNGGIVAANVIVLLIALLGFLWFAY 265 : : : : : : : : : : : : : : :
QY	263 RKGYFSKTSFKFSSSKATMTSENDFKHKSPII 298 : : : : : : : : : : : : : : :
Db	266 SRGYLDRKEN-KKIYQSPSETRSKKNFQQTSFLV 300 : : : : : : : : : : : : : : :
RESULT 12	
QZWT0	PRELIMINARY; PRT; 289 AA.
ID	QZWT0;
AC	QZWT0;
DT	01-JUN-2003 (TE=EMBLrel. 24, Created)
DT	01-JUN-2003 (TE=EMBLrel. 24, Last sequence update)
DT	01-OCT-2003 (TE=EMBLrel. 25, Last annotation update)
DS	Similar to junctional adhesion molecule 1.
OS	Xenopus laevis (African clawed frog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Ampibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC	Xenopodinae; Xenopus.
OX	NCB_I_TaxID=8355;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Embryo;
RA	Klein S., Strausberg R.; Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR	EMBL; BC046720; AAH46720.1; -
DR	InterPro; IPR003599; Ig_
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003598; Ig_c2.
DR	Pfam; PF00047; ig; 2.

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QY 4 RSRRLRLRLRLRLVVALGYHAYGSAFKDQVWVAVYQEAAILACKTKPKTVXSLEW 63
DB 6 KAGRKLFLFTSMILGSLVQKGSVYTAQSDVQPE-----NESIKLTCTYSGFSSPRVW 61
QY 64 KKL-GRSVSFVYQTLQDGFKNRAEMIDFNIRIKNTRSDAGKYRCEVSAPSGQGNLE 122
DB 62 KFGQSTTALVCYNSQITAPVADRVTFFSSSGITFSSVTRKDNGETWVS--EEGGQNYG 119
QY 123 EDTVLEVLVAVPAPSCVPSALSCTVVELRCDQKGNPAPETWFKDGIRLLENPLRG 182
DB 120 EVSIHLATVLPSPKPTTISVPSVTIGNRAVLTCSEHDGSPSEYSWFKDGISMLTADAKK 179
QY 183 SQS--TNSSTYNTWTKTGTQFNVTGKLDTGCEYSCEARNVSVG--YRCPGKRQVDDNLNSGI 240
DB 180 TRAFNNSFTIDPKSGDLIFPVTAFDSGEYVCOQNGYGTAMRSEAAHMDAVELNVGGI 239
QY 241 IAAVVVALVTSVCGLVGCYVQAKGYF---SKETSFOKSNSSSKATTMSNDPKHTKXFI 297
DB 240 VAAVLVTLILGLLIFGVWFAYSRGYFERTKKGTAQPKKVIYQSPSTRSEGEFKQTSSFL 299
QY 298 I 298
DB 300 V 300

RESULT 14
Q9JHY1 PRELIMINARY; PRT; 300 AA.
AC Q9JHY1
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Junctional adhesion molecule JAM.
GN JAM.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague Dawley;
RA Mashima H., Kojima I.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF276998; AAF78250.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
SQ SEQUENCE 300 AA; 32369 MW; 45AE362A96158BFA CRC64;

Query Match 26.9%; Score 409.5; DB 11; Length 300;
Best Local Similarity 34.3%; Pred. No. 4.8e-30;
Matches 95; Conservative 49; Mismatches 98; Indels 35; Gaps 6;

QY 28 GFSAKPKDQVWVAVYQEAAILACKTKPKTVXSLEWKL-GRSVSFVYQTLQDGFKNR 86
DB 53 GFSP-----RVEWKFVQGSTTALVCYNNQITVFIADR 85
QY 87 AEMIDFNIRIKNTRSDAGKYRCEVSAPSGQGNLEEDTVTLVAVPAPSCVPSALS 146
DB 86 VTSSSGITFSSVTRKDNGETWVS--EDGGQNGEVSIIHLTVLPSPKPTTISVPSVT 143
QY 147 SGTVELRCODKGNPAPETWFKDGIRLLENPLRGQS--TNSSTYNTWTKTGTQFNVT 205
DB 144 IGRNAVLTCSHDGSPSEYSWFKDGVMPLTADAKTRAFINSYTIIDPKSGDLVFDVPS 203
QY 206 KLDTGCEYSCEARNVSVG--YRCPGKRQVDDNLNSGIIAAVVVALVTSVCGLVGCYVQAK 264
DB 204 AFDSGEYVCAQNGYGTAMRSEAVRMEAVELNVGGIVAALVTLILGLLIFGVWFAYSR 263
QY 265 GYF---SKETSFOKSNSSSKATTMSNDPKHTKXFI 298
DB 265 GYF---SKETSFOKSNSSSKATTMSNDPKHTKXFI 298
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DB 264 GYFERTKGTAPKPKVIYQSPARSEGEFKQTSSFLV 300

RESULT 15
Q9Y5B2 PRELIMINARY; PRT; 259 AA.
AC Q9Y5B2
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Junctional adhesion molecule.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu Y., Nusrat A., Schnell F.J., Walsh S., Reaves T.A., Pochet M.,
RA Foley C., Parkos C.A.;
RT "Human junctional adhesion molecule is expressed by polarized columnar
RT epithelia and regulates tight junction resealing";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF154005; AAD43794.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 259 AA; 28122 MW; FE38521A911562D0 CRC64;

Query Match 25.9%; Score 393.5; DB 4; Length 259;
Best Local Similarity 36.9%; Pred. No. 1.2e-28;
Matches 87; Conservative 41; Mismatches 97; Indels 11; Gaps 4;

QY 59 SVSFVYQTLQDGFKNRAEMIDFNIRIKNTRSDAGKYRCEVSAPSGQGNLEEDTVTL 128
DB 29 SCAYSGFSPPRAASYEDRVTFELTGITPKSVTRBDTGTTCMTF--BEGGNSYGEVKVKL 86
QY 129 EVLVAPAPSCVPSALSCTVVELRCODKGNPAPETWFKDGIRLLENPLRGQSNTS 188
DB 87 IVLVPPSKPTVINPSSAIGNRAVLTCSEQDGSPPSEYTWFKDGIWMPNPKSTRAFNS 146
QY 189 SYTMNTKGTGTQFNVTGKLDTGCEYSCEARNVSVGYRRCPGK-RMQVDDNLNSGIIAVVVV 247
DB 147 SYVLNPTTGELVDFDPLSASDTGEYSCEARNGYGTPTMTSNVAVRMEAVERNVGVIAAVLVT 206
QY 248 ALVTSVCGLVGCYVQAKGYFSKETSFOKSNSSSKA-----TTMSNDPKHTKXFI 298
DB 207 LILGLIFGVWFAYSRGHFDRP---KKGTSKKVIYQSPARSEGEFKQTSSFLV 259

Search completed: July 15, 2004, 23:54:29
Job time : 54.5882 secs
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OM protein - protein search, using sw model

Run on: July 15, 2004, 23:48:38 ; Search time 19.7112 Seconds
(without alignments)
1089.410 Million cell updates/sec

Title: US-09-852-797-76_COPY_23_98

Perfect score: 388

Sequence: 1 YKAYGFSAPKQQVTVAVX.....LQDGFKNRAEMIDFNIRIKN 76

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:.*
1: Geneseq1990s:.*
2: Geneseq1990s:.*
3: Geneseq2000s:.*
4: Geneseq2001s:.*
5: Geneseq2002s:.*
6: Geneseq2003as:.*
7: Geneseq2003bs:.*
8: Geneseq2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	385	99.2	235	6 AAO30179	Human nov
2	385	99.2	298	2 AAW85457	Secreted
3	385	99.2	298	4 AAU00512	Human jun
4	385	99.2	298	5 ABP61801	Human pol
5	385	99.2	298	6 ABR58532	Human vas
6	385	99.2	298	6 AAO16452	Human jun
7	385	99.2	303	4 AAM23693	Human EST
8	385	99.2	312	2 AAY23324	A33 relat
9	385	99.2	312	2 AAY08060	Human PRO
10	385	99.2	312	2 AAU13354	Amino aci
11	385	99.2	312	3 AAB33421	Human PRO
12	385	99.2	312	3 AAY70668	Human PRO
13	385	99.2	312	3 AAB24401	Human PRO
14	385	99.2	312	3 ADC78384	Human PRO
15	385	99.2	312	4 AAB80222	Human PRO
16	385	99.2	312	4 AAU00821	Human imm
17	385	99.2	312	4 AAU12339	Human PRO
18	385	99.2	312	4 AAB53081	Human ang
19	385	99.2	312	6 AABU71600	Human PRO
20	385	99.2	312	6 ABO17783	Novel hum
21	385	99.2	312	6 ABU17455	Human PRO
22	385	99.2	312	6 ABU81037	Human PRO
23	385	99.2	312	6 ABU17901	Human sec
24	385	99.2	312	6 ABO01784	Novel hum
25	385	99.2	312	6 ABU66737	Human PRO

26	385	99.2	312	6 ABU54357	Human sec
27	385	99.2	312	6 ABO47372	Human sec
28	385	99.2	312	6 ABU59818	Novel sec
29	385	99.2	312	6 ABO25008	Human sec
30	385	99.2	312	6 ABU64509	Human sec
31	385	99.2	312	6 ABU67355	Human sec
32	385	99.2	312	6 ABO14875	Human sec
33	385	99.2	312	6 ABU07738	Human A-3
34	385	99.2	312	6 ABU67013	Human sec
35	385	99.2	312	6 ABU69632	Novel hum
36	385	99.2	312	6 ABO14814	Human sec
37	385	99.2	312	6 ADA45855	Novel hum
38	385	99.2	312	6 ADA76286	Human PRO
39	385	99.2	312	6 ADB29269	Human sec
40	385	99.2	312	6 ADA18936	Human PRO
41	385	99.2	312	6 ADA61559	Homo sapi
42	385	99.2	312	6 ADB19344	Novel hum
43	385	99.2	312	6 ADB27885	Human PRO
44	385	99.2	312	6 ADA86364	Novel hum
45	385	99.2	312	6 ADB15928	Human PRO

ALIGNMENTS

RESULT 1
AAO30179
ID AAO30179 standard; protein; 235 AA.

XX AC AAO30179;
XX DT 03-SEP-2003 (first entry)
XX DE Human novel splice variant of VEJAM (NOJAM).

XX KW Human; forensic analysis; chromosome marker; organelle-specific marker;
XX KW novel-related disorder; neurological disorder; gene therapy; nootropic;
XX KW neuroprotective; vascular endothelial junctional adhesion molecule;
XX KW VEJAM; NOJAM.

XX OS Homo sapiens.
XX OS Synthetic.

XX FH Key Location/Qualifiers
XX FT Peptide 1..28
XX FT /label= Signal_peptide
XX FT Protein 29..235
XX FT /note= "Human mature NOJAM protein"

XX WO2003046180-A2.

XX PD 05-JUN-2003.

XX PF 25-NOV-2002; 2002WO-EP013210.

XX PR 28-NOV-2001; 2001US-0334147P.

XX PR 14-DEC-2001; 2001US-0340465P.

XX PR 18-APR-2002; 2002US-0373947P.

XX PA (GEST) GENSET SA.

XX PI Bejanin S, Tanaka H;

XX XX WPI; 2003-505202/47.

XX DR N-PSDB; AAL60897.

XX PT New isolated polynucleotides and polypeptides useful as reagents in

XX PT forensic analyses, as chromosome markers, as tissue/cell/organelle-

XX PT specific markers, in producing expression vectors, or in screening and

XX PT diagnostic assays.

XX PS Claim 2; Page 229; 242pp; English.

CC The invention relates to human novel polynucleotide and polypeptide
 CC sequences useful as reagents in forensic analyses, as chromosome markers,
 CC as tissue/cell/organelle-specific markers, in producing expression
 CC vectors, or in screening and diagnostic assays. The invention is used as
 CC reagents in screening and diagnostic assays for abnormal novel expression
 CC and/or biological activity, and in screening compounds that may be used
 CC in the treatment of novel-related disorders, e.g. neurological disorders.
 CC The novel gene is also used in gene therapy. The present sequence is
 CC human novel splice variant of vascular endothelial junctional adhesion
 CC molecule (VEJAM), NOJAM of the invention
 CC
 XX Sequence 235 AA;

Query Match 99.2%; Score 385; DB 6; Length 235;
 Best Local Similarity 97.4%; Pred. No. 3.9e-45;
 Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YHKAYGFSAPKDDQVVTA VXXQEA I LACKTPKKT VXSRLWKLG RSVSFVYYQQT LQGD 60
 DB 23 YHKAYGFSAPKDDQVVTA VXEYQEA I LACKTPKKT VSSRLWKLG RSVSFVYYQQT LQGD 82

QY 61 FKQRAEMIDFNIRIKN 76
 DB 83 FKQRAEMIDFNIRIKN 98

RESULT 2
 AA085457
 ID AA085457 standard; protein; 298 AA.
 XX
 AC AA085457;
 XX
 DT 25-FEB-1999 (first entry)
 XX
 DE Secreted protein encoded by clone ct864_4.
 XX
 KW Secreted protein; nutritional activity; immune stimulating; vaccine;
 KW suppressing activity; haematopoiesis regulating activity;
 KW tissue growth activity; activin; inhibin activity; chemotaxis;
 KW chemokinetic activity; haemostasis; thrombolytic activity; receptor;
 KW ligand; anti-inflammatory; cadherin; tumour invasion suppressor;
 KW tumour inhibition; gene therapy.
 XX
 OS Homo sapiens.
 XX
 FN WO9842739-A2.
 XX
 PD 01-OCT-1998.
 XX
 XX 20-MAR-1998; 98WO-US005653.
 PF
 PR 21-MAR-1997; 97US-00822167.
 PR 19-MAR-1998; 98US-00044466.
 XX
 PA (GEMY) GENETICS INST INC.
 XX
 XX Jacobs K, McCoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
 PI Spaulding V, Agostino MJ;
 XX
 DR WPI; 1998-609890/51.
 DR N-PSDB; AAV82780.

New polynucleotides encoding secreted human proteins - derived from human
 PT foetal brain, adult brain, foetal kidney, placenta or adult pineal gland
 PT cDNA libraries.

PS Claim 17; Page 73-74; 113pp; English.

XX The present sequence represents a secreted protein. The polynucleotide
 CC and secreted protein are predicted to have biological activities which
 CC would make them suitable for treating, preventing or ameliorating medical
 CC conditions in humans and animals, although no supporting data is given.
 CC Suggested activities include nutritional activity, immune stimulating

CC (e.g. as vaccines) or suppressing activity, haematopoiesis regulating
 CC activity, tissue growth activity, activin/inhibin activity,
 CC chemotactic/chemokinetic activity, haemostatic and thrombolytic activity,
 CC receptor/ligand activity, anti-inflammatory activity, cadherin/tumour
 CC invasion suppressor activity, and tumour inhibition activity (no data is
 CC given in the specification to support these activities). The
 CC polynucleotide is also stated to be useful for gene therapy
 XX
 XX Sequence 298 AA;

Query Match 99.2%; Score 385; DB 2; Length 298;
 Best Local Similarity 97.4%; Pred. No. 5.2e-45;
 Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YHKAYGFSAPKDDQVVTA VXXQEA I LACKTPKKT VXSRLWKLG RSVSFVYYQQT LQGD 60
 DB 23 YHKAYGFSAPKDDQVVTA VXEYQEA I LACKTPKKT VSSRLWKLG RSVSFVYYQQT LQGD 82

QY 61 FKQRAEMIDFNIRIKN 76
 DB 83 FKQRAEMIDFNIRIKN 98

RESULT 3
 AAU00512
 ID AAU00512 standard; protein; 298 AA.

XX
 AC AAU00512;
 XX
 DT 09-MAY-2001 (first entry)
 XX
 DE Human junctional adhesion protein (JAM2).

XX Junctional adhesion protein; JAM2; cellular localisation;
 KW cellular expression; immunoprecipitation; stroke; phosphorylation;
 KW glycosylation; paracellular migration; inflammatory disease; arthritis;
 KW asthma; rheumatoid arthritis; inflammatory bowel disease;
 KW Crohn's disease.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..28
 FT /note= "Possible signal peptide #2"
 FT Peptide 1..20
 FT /note= "Possible signal peptide #1"
 FT Protein 21..298
 FT /note= "Possible mature JAM2 #1"
 FT Protein 29..298
 FT /note= "Possible mature JAM2 #2"
 FT Domain 237..254
 FT /note= "Transmembrane domain"

XX WO200114404-A1.

XX 01-MAR-2001.

XX 23-AUG-2000; 2000WO-US023158.

XX 24-AUG-1999; 99US-0150459P.

XX (TEXA-) TEXAS BIOTECHNOLOGY CORP.

XX Cunningham S, Trindad Arrate Barros M;
 PI N-PSDB; AAS00512.

XX WPI; 2001-218425/22.

XX Novel nucleic acids encoding human junctional adhesion protein useful for
 PT producing antibodies that are suitable for therapeutic purposes.

XX Claim 4; Page 46-47; 51pp; English.

CC The sequence represents a human functional adhesion molecule 2 (JAM2).
CC The polynucleotide encoding the polypeptide is useful for recombinant
CC production of JAM-2 protein, which in turn is useful for the production
CC of antibodies. The antibodies may be used for probing cellular
CC localisation and/or expression of JAM2 in tissues under normal and
CC disease states, for immunoprecipitating JAM2 protein from cells and/or
CC stroke tissues to determine whether it is modified by glycosylation and
CC phosphorylation, and for determining JAM2 function. The antibodies
CC inhibit interaction of JAM2 with inflammatory cells or influences their
CC paracellular migration, and is therefore useful for alleviating
CC inflammatory diseases such as arthritis, asthma, rheumatoid arthritis,
CC inflammatory bowel disease and Crohn's disease
XX
SQ Sequence 298 AA;
Query Match 99.2%; Score 385; DB 4; Length 298;
Best Local Similarity 97.4%; Pred. No. 5.2e-45;
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 YHKAYGFSAPKDDQVVTAVYQEAAILACKTPKTKVXSRLEWKKLGRSVSFYVYQQTLOGD 60
DQ 23 YHKAYGFSAPKDDQVVTAVYQEAAILACKTPKTKVXSRLEWKKLGRSVSFYVYQQTLOGD 82
QY 61 FKNRAEMIDFNIRIKN 76
DQ 83 FKNRAEMIDFNIRIKN 98
RESULT 4
ABP61801 standard; protein; 298 AA.
XX AC ABP61801;
XX DT 04-OCT-2002 (first entry)
XX DE Human polypeptide SEQ ID NO 155.
XX KW Human; cytostatic; antirheumatic; antiarthritic; vulnary; analgesic;
KW antiinflammatory; antibacterial; immunosuppressive; antiparkinsonian;
KW neuroprotective; nootropic; osteopathic; haemostatic; vasotropic;
KW antitumor; fungicide; antidiabetic; antiasthmatic; antiallergic;
KW immunostimulant; antiparasitic; secreted protein; transmembrane protein;
KW cytokine; cell proliferation; cell differentiation; autoimmune disease;
KW stem cell; growth factor; nervous system disease; neuropathy;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease;
KW osteoporosis; severe combined immunodeficiency; SCID; infection;
KW multiple sclerosis; rheumatoid arthritis; gene therapy.
XX OS Homo sapiens.
XX PN US2002065394-A1.
XX PD 30-MAY-2002.
XX PF 22-DEC-2000; 2000US-00745763.
XX PR 18-MAR-1998; 98US-00040963.
XX PA (JACO/) JACOBS K.
XX PA (MCCO/) MCCOY J M.
XX PA (LAVA/) LAVALLIE E R.
XX PA (COLL/) COLLINS-RACIE L A.
XX PA (EVAN/) EVANS C.
XX PA (NERB/) MERBERG D.
XX PA (TREA/) TREACY M.
XX PA (SPAU/) SPAULDING V.
XX Jacobs K, Mccoy JM, Lavallie ER, Collins-Racie LA, Evans C;
XX Merberg D, Treacy M, Spaulding V;
XX WPI: 2002-582343/62.
XX N-PSDB; ABQ92017.

XX Novel secreted or transmembrane protein and polynucleotide encoding the
PT protein, useful for diagnosis and treatment of neurological disorders,
PT cancer, autoimmune diseases, bone disorders and lung or liver fibrosis.
XX
PS Claim 54; Page 116-117; 284pp; English.
XX The invention relates to human secreted or transmembrane protein (I),
CC their fragments and is encoded by specific complementary deoxyribonucleic
CC acid (cDNA) inserts (II), where the protein is substantially free from
CC other mammalian proteins. (I) are useful for preventing, treating or
CC ameliorating a medical condition, especially immunological treatment or
CC prevention of tumours. (I) exhibits activity relating to angiogenesis,
CC cytokine, cell proliferation, cell differentiation, antiinflammatory,
CC stem cell growth factor activity and activin or inhibin-related
CC activities. (I) can be used to manipulate stem cells in culture to give
CC rise to neuroepithelial cells that can be used to augment or replace
CC cells damaged by illness, autoimmune disease, accidental damage or
CC genetic disorders. (I) induces the proliferation of neural cells and
CC regeneration of nerve and brain tissue and is useful for the treatment of
CC central and peripheral nervous system diseases and neuropathies, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis. (I) is involved in chemotactic or chemokinetic
CC activity, regulation of haematopoiesis and is useful for treating myeloid
CC or lymphoid cell disorders, platelet disorders such as thrombocytopaenia
CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
CC tissue growth and in tissue repair, healing of burns, incisions, ulcers,
CC for treating osteoporosis, osteoarthritis, bone degenerative disorders or
CC periodontal disease. (I) is also useful for gut protection or
CC regeneration and treatment of lung or liver fibrosis, reperfusion injury
CC in various tissues, various immune deficiencies and disorders including
CC severe combined immunodeficiency (SCID), bacterial or fungal infections,
CC autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis,
CC diabetes mellitus, myasthenia gravis, allergic reactions and conditions,
CC such as asthma or other respiratory problems. (II) is useful to express
CC recombinant protein, as markers for tissues in which the corresponding
CC protein is preferentially expressed and in gene therapy. The present
CC sequence is that of a polypeptide of the invention
XX
SQ Sequence 298 AA;
Query Match 99.2%; Score 385; DB 5; Length 298;
Best Local Similarity 97.4%; Pred. No. 5.2e-45;
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 YHKAYGFSAPKDDQVVTAVYQEAAILACKTPKTKVXSRLEWKKLGRSVSFYVYQQTLOGD 60
DQ 23 YHKAYGFSAPKDDQVVTAVYQEAAILACKTPKTKVXSRLEWKKLGRSVSFYVYQQTLOGD 82
QY 61 FKNRAEMIDFNIRIKN 76
DQ 83 FKNRAEMIDFNIRIKN 98
RESULT 5
ABR58532 standard; protein; 298 AA.
XX ID ABR58532
XX AC ABR58532;
XX DT 09-JUL-2003 (first entry)
XX DE Human vascular endothelial junction-associated molecule protein.
XX KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
KW heart disease; atherosclerosis; endometriosis.
XX OS Homo sapiens.
XX PN WO2003025138-A2.
XX PD 27-MAR-2003.
XX

```
PF 17-SEP-2002; 2002WO-US029560.
XX
XX 17-SEP-2001; 2001US-0323469P.
PR 20-SEP-2001; 2001US-0323887P.
PR 13-NOV-2001; 2001US-0350666P.
PR 08-FEB-2002; 2002US-0355145P.
PR 08-FEB-2002; 2002US-0355257P.
PR 12-APR-2002; 2002US-0372246P.
XX
XX (EOSB-) EOS BIOTECHNOLOGY INC.
PA
XX
XX Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
PI Zlotnick A;
XX
XX WPI; 2003-354600/33.
DR N-PSDB; ACC72652.
XX
XX New genes that are up-regulated or down-regulated in cancers, useful as
PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
PT therapeutic targets for screening drugs for treating these diseases.
XX
XX Claim 12; Page 149; 767pp; English.
XX
XX The present invention describes an isolated nucleic acid molecule, which
CC comprises the sequence of any of the genes that are up-regulated or down-
CC regulated in specific cancers (e.g. about 1031 genes up-regulated in
CC acute lymphocytic leukemia). ACC72641 to ACC72680 represent cancer-
CC related gene nucleotide sequences which encode the proteins given in
CC ABR58521 to ABR58709. Also described: (1) determining the presence or
CC absence of a pathological cell in a patient; (2) an expression vector
CC comprising a nucleic acid molecule described above; (3) a host cell
CC comprising the vector; (4) an isolated polypeptide, which is encoded by
CC the nucleic acid; (5) an antibody that specifically binds the polypeptide
CC of (4); (6) specifically targeting a compound to a pathological cell in a
CC patient by administering to the patient the antibody above; and (7) a
CC drug screening assay. The nucleic acid is useful as diagnostic markers or
CC therapeutic targets. In particular, the nucleic acid is useful for
CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
CC atherosclerosis and endometriosis. The nucleic acid is also useful in
CC drug screening, particularly for identifying agents for treating these
CC pathologies
XX
XX Sequence 298 AA;
SQ
Query Match 99.2%; Score 385; DB 6; Length 298;
Best Local Similarity 97.4%; Pred. No. 5.2e-45;
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 YHKAYGFSAPKDDQVVTA VYQAEILACKTPKKT VXSRLWKLGSRVSFVYQQTLOGD 60
Db 23 YHKAYGFSAPKDDQVVTA VYQAEILACKTPKKT VXSRLWKLGSRVSFVYQQTLOGD 82
QY 61 FKNRAEMIDFNIRIKN 76
Db 83 FKNRAEMIDFNIRIKN 98
RESULT 6
AAO16452
ID AAO16452 standard; protein; 298 AA.
XX
XX AAO16452;
AC
XX
XX 17-APR-2003 (first entry)
DT
XX
XX Human junctional adhesion molecule 2 (huJAM2).
DE
XX Human; gene therapy; extracellular region; junctional adhesion molecules;
KW huJAM; immune system disorder; immune deficiency; autoimmune disorder;
KW inflammatory disorder; cancer; wound healing; cardiovascular disease;
KW full-length membrane-bound huJAM protein.
KW
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```
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..28
FT Protein /label= Signal_peptide
FT Domain /note= "Mature huJAM2"
FT /note= "Extracellular domain; Specifically claimed region"
XX
XX WO2003008541-A2.
XX
XX 30-JAN-2003.
XX
XX 05-JUL-2002; 2002WO-US019800.
XX
XX 16-JUL-2001; 2001US-0305752P.
PR 05-FEB-2002; 2002US-0354345P.
XX
XX (ELIL ) LILLY & CO ELI.
PA
XX
XX Heuer JG, Smith RC, Su EW;
PI
XX WPI; 2003-221848/21.
DR N-PSDB; AAL51599.
XX
XX New extracellular human junctional adhesion molecule (huJAM) polypeptide,
PT useful for treating an immune system disorder such as an immune
PT deficiency or an inflammatory disorder, cancer, wound healing, or a
PT cardiovascular disease.
XX
XX Disclosure; Fig 1; 131pp; English.
XX
XX The invention comprises the DNA and protein sequences of the
CC extracellular region of human junctional adhesion molecules (huJAM). The
CC extracellular huJAM DNA and protein sequences are useful in the treatment
CC of: immune system disorders (e.g. immune deficiency); autoimmune
CC disorders; inflammatory disorders; cancer; wound healing; or a
CC cardiovascular disease. The present amino acid sequence represents the
CC full-length membrane-bound huJAM2 protein
XX
XX Sequence 298 AA;
SQ
Query Match 99.2%; Score 385; DB 6; Length 298;
Best Local Similarity 97.4%; Pred. No. 5.2e-45;
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 YHKAYGFSAPKDDQVVTA VYQAEILACKTPKKT VXSRLWKLGSRVSFVYQQTLOGD 60
Db 23 YHKAYGFSAPKDDQVVTA VYQAEILACKTPKKT VXSRLWKLGSRVSFVYQQTLOGD 82
QY 61 FKNRAEMIDFNIRIKN 76
Db 83 FKNRAEMIDFNIRIKN 98
RESULT 7
AAM23693
ID AAM23693 standard; protein; 303 AA.
XX
XX AAM23693;
AC
XX
XX 12-OCT-2001 (first entry)
DT
XX
XX Human EST encoded protein SEQ ID NO: 1218.
DE
XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
KW gene therapy; nutrition.
XX
```



```

OS Homo sapiens.
XX WO200154477-A2.
XX PD 02-AUG-2001.
XX PF 25-JAN-2001; 2001WO-US002887.
XX PR 25-JAN-2000; 2000US-00491404.
XX PR 17-JUL-2000; 2000US-00617746.
XX PR 03-AUG-2000; 2000US-00631451.
XX PR 15-SEP-2000; 2000US-00663870.
XX PA (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V,
XX Cao Y, Dmanac RA, Zhang J, Werhman T;
XX WPI; 2001-476164/51.
XX N-PSDB; AAH98352.
XX Isolated polypeptide for treatment of diseases, diagnostics, raising
XX antibodies and research use.
XX Claim 20; Page 878-879; 1275pp; English.
XX The present invention provides the protein and coding sequences of novel
XX proteins from a variety of organisms, including human, dog, cat, horse,
XX cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
XX urchin and tomato. These were derived from expressed sequence tags (ESTs)
XX from the organism of interest. They can be used in diagnostics,
XX forensics, gene mapping, identification of mutations, to assess
XX biodiversity and for nutritional purposes. The present sequence is a
XX protein of the invention
XX Sequence 303 AA;
XX
XX Query Match          99.2%; Score 385; DB 4; Length 303;
XX Best Local Similarity 97.4%; Pred. No. 5.3e-45;
XX Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1 YHKAYGFSAPKQQVVTAVYQEAAILACKTPKTVXSRLEWKLGSRVSFVYQQTLOGD 60
XX Db 23 YHKAYGFSAPKQQVVTAVYQEAAILACKTPKTVXSRLEWKLGSRVSFVYQQTLOGD 82
XX
XX QY 61 FKNRAEMIDFNIRIKN 76
XX Db 83 FKNRAEMIDFNIRIKN 98
XX
XX RESULT 8
XX ID AAY23324
XX AC AAY23324 standard; protein; 312 AA.
XX XX AAY23324;
XX DT 02-SEP-1999 (first entry)
XX DE A33 related antigen PRO245.
XX DE A33 related antigen; PRO301; PRO362; PRO245; inflammatory disease;
XX tumor.
XX OS Homo sapiens.
XX XX
XX PN WO9927098-A2.
XX PD 03-JUN-1999.
XX XX
XX PF 20-NOV-1998; 98WO-US024855.
XX XX
XX PR 21-NOV-1997; 97US-0066364P.
XX PR 20-MAR-1998; 98US-0078936P.

```

```

PR 17-SEP-1998; 98WO-US019437.
XX (GETH ) GENENTECH INC.
XX Ashkenazi A, Fong S, Goddard A, Gurney AL, Napier MA, Tumas D;
XX Wood WI;
XX WPI; 1999-404743/34.
XX N-PSDB; AAX81770.
XX Antigen PRO301, PRO362 and PRO245 related to A33.
XX Example 3; Fig 11; 122pp; English.
XX
XX The specification describes A33 related antigens PRO301, PRO362 and
XX PRO245. The methods and compositions of the invention are useful for the
XX treatment and diagnosis of inflammatory disease and tumours in mammals.
XX Such inflammatory diseases include of inflammatory bowel disease,
XX systemic lupus erythematosus, rheumatoid arthritis, juvenile chronic
XX arthritis, spondyloarthropathies, systemic sclerosis, scleroderma,
XX idiopathic inflammatory myopathies, dermatomyositis, polymyositis,
XX Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune hemolytic
XX anemia, immune pancytopenia, paroxysmal nocturnal hemoglobinuria,
XX autoimmune thrombocytopenia, idiopathic thrombocytopenic purpura, immune-
XX mediated thrombocytopenia, thyroiditis, Grave's disease, Hashimoto's
XX thyroiditis, juvenile lymphocytic thyroiditis, atrophic thyroiditis,
XX diabetes mellitus, immune-mediated renal disease, glomerulonephritis,
XX tubulointerstitial nephritis, demyelinating diseases of the central and
XX peripheral nervous systems such as multiple sclerosis, idiopathic
XX polyneuropathy, hepatobiliary diseases, infectious hepatitis A, B, C, D,
XX E, nonhepatotropic viruses, autoimmune chronic active hepatitis, primary
XX biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
XX inflammatory and fibrotic lung diseases, gluten-sensitive enteropathy,
XX Whipple's disease, autoimmune or immune-mediated skin diseases allergic
XX diseases of the lung such as eosinophilic pneumonias, idiopathic
XX pulmonary fibrosis and hypersensitivity pneumonitis transplantation
XX associated diseases disease. The present sequence represents PRO245
XX
XX Sequence 312 AA;
XX
XX Query Match          99.2%; Score 385; DB 2; Length 312;
XX Best Local Similarity 97.4%; Pred. No. 5.5e-45;
XX Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1 YHKAYGFSAPKQQVVTAVYQEAAILACKTPKTVXSRLEWKLGSRVSFVYQQTLOGD 60
XX Db 23 YHKAYGFSAPKQQVVTAVYQEAAILACKTPKTVXSRLEWKLGSRVSFVYQQTLOGD 82
XX
XX QY 61 FKNRAEMIDFNIRIKN 76
XX Db 83 FKNRAEMIDFNIRIKN 98
XX
XX RESULT 9
XX ID AAY08060
XX AC AAY08060 standard; protein; 312 AA.
XX XX AAY08060;
XX DT 11-SEP-2000 (first entry)
XX DE Human PRO245 protein.
XX XX
XX KW Inflammatory cell infiltration; immune response; T cell proliferation;
XX anti-inflammatory; anti-autoimmune; anti-diabetic; spondyloarthopathy;
XX T cell-mediated disease; spondyloarthopathy; sclerosis; renal disease;
XX inflammatory myopathy; hemolytic anemia; thrombocytopenia; thyroiditis;
XX diabetes mellitus; demyelinating polyneuropathy; Guillain-Barre syndrome;
XX multiple sclerosis; polyneuropathy; hepatitis; cirrhosis; enteropathy;
XX sclerosing cholangitis; inflammatory bowel disease; Whipple's disease;
XX skin disease; dermatitis; psoriasis; asthma; allergic rhinitis; tumor;
XX food hypersensitivity; urticaria; eosinophilic pneumonia; transplant;
XX idiopathic pulmonary fibrosis; graft rejection; PRO245; human.

```


PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-NOV-1997; 97US-0066840P.
XX (GETH) GENENTECH INC.
XX
XX Wood WI, Gurney AL, Goddard A, Pennica D, Chen J, Yuan J;
XX WPI; 1999-229533/19.
XX N-PSDB; AAX52225.
XX
XX New isolated human genes and polypeptides used in, e.g. treatment of
XX Gastrointestinal ulceration.
XX
XX Claim 12; Fig 24; 320pp; English.
XX
XX AAY13344-403 represent secreted and transmembrane human proteins. The
XX cDNA sequences are obtained from cDNA libraries, prepared from fetal
XX lung, fetal kidney, fetal brain, fetal liver and fetal retina. The
XX encoded polypeptides have specific uses based on their homology to known
XX polypeptides, e.g. PRO211 and PRO217 can be used for disorders associated
XX with the preservation and maintenance of gastrointestinal mucosa and the
XX repair of acute and chronic mucosal lesions (e.g. enterocolitis,
XX Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital
XX microvillus atrophy), skin diseases associated with abnormal keratinocyte
XX differentiation (e.g. psoriasis, epithelial cancers such as lung squamous
XX cell carcinoma of the vulva and gliomas), potent effects on cell growth
XX and development, diseases related to growth or survival of nerve cells
XX including Parkinson's disease, Alzheimer's disease, ALS, neuropathies or
XX cancer. PRO265 can be used as for fibromodulin, e.g. for reducing dermal
XX scarring. PRO264 can be used as a target for anti-tumor drugs. PRO533 may
XX be used in the treatment of Usher Syndrome or Atrophia areata; PRO269 can
XX be used as an anti-thrombotic agent; PRO287 polypeptides and portions may
XX have therapeutic applications in wound healing and tissue repair; PRO317
XX can be used for treating problems of the kidney, uterus, endometrium,
XX blood vessels, or related tissue, e.g. in the heart of genital tract
XX
XX SQ Sequence 312 AA;

Query Match 99.2%; Score 385; DB 2; Length 312;
Best Local Similarity 97.4%; Pred. No. 5.5e-45;
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YHKAYGFSAPKQOVVTAVYQEAIIACKTPKTYXSRLEWKKLGSRVSFVYVYQOTLQGD 60
Db |||||||
23 YHKAYGFSAPKQOVVTAVYQEAIIACKTPKTYXSRLEWKKLGSRVSFVYVYQOTLQGD 82

QY 61 FKGRAEMIDFNIRKN 76
Db |||||||
83 FKGRAEMIDFNIRKN 98

RESULT 11
AAB33421
ID AAB33421 standard; protein; 312 AA.
XX
XX AAB33421;
XX
XX 29-JAN-2001 (first entry)
XX
XX Human PRO245 protein UNQ219 SEQ ID NO:36.
XX
XX Human; immune related disease; diagnosis; antiinflammatory; cardiant;
XX dermatological; antiarthritic; antirheumatic; immunosuppressive;
XX haemostatic; antithyroid; antidiabetic; neuroprotective;
XX antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;

KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW osteoarthritis; spondyloarthritis; systemic sclerosis; sarcoidosis;
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW autoimmune thrombocytopenia; immune-mediated renal disease;
KW demyelinating disease; hepatobiliary disease; Whipple's disease;
KW inflammatory bowel disease; gluten-sensitive enteropathy;
KW autoimmune disease; immune-mediated skin disease; allergic disease;
KW immunological disease; transplantation associated disease;
KW graft rejection; graft-versus-host-disease.
XX Homo sapiens.
XX OS
XX PN WO200053758-A2.
XX PD 14-SEP-2000.
XX XX
XX PF 02-MAR-2000; 2000WO-US005841.
XX PR 08-MAR-1999; 99WO-US005028.
XX PR 10-MAR-1999; 99US-0123618P.
XX PR 12-MAR-1999; 99US-0123957P.
XX PR 23-MAR-1999; 99US-0125775P.
XX PR 12-APR-1999; 99US-0128849P.
XX PR 20-APR-1999; 99WO-US008615.
XX PR 28-APR-1999; 99US-0131445P.
XX PR 04-MAY-1999; 99US-0132371P.
XX PR 14-MAY-1999; 99US-0134287P.
XX PR 02-JUN-1999; 99WO-US012252.
XX PR 23-JUN-1999; 99US-0141037P.
XX PR 20-JUL-1999; 99US-0144758P.
XX PR 26-JUL-1999; 99US-0145698P.
XX PR 28-JUL-1999; 99US-0146222P.
XX PR 01-SEP-1999; 99WO-US020111.
XX PR 08-SEP-1999; 99WO-US020594.
XX PR 13-SEP-1999; 99WO-US020944.
XX PR 15-SEP-1999; 99WO-US021090.
XX PR 15-SEP-1999; 99WO-US021547.
XX PR 05-OCT-1999; 99WO-US023089.
XX PR 29-OCT-1999; 99US-0162506P.
XX PR 29-NOV-1999; 99WO-US028214.
XX PR 30-NOV-1999; 99WO-US028313.
XX PR 30-NOV-1999; 99WO-US028409.
XX PR 01-DEC-1999; 99WO-US028301.
XX PR 01-DEC-1999; 99WO-US028634.
XX PR 02-DEC-1999; 99WO-US028551.
XX PR 02-DEC-1999; 99WO-US028564.
XX PR 16-DEC-1999; 99WO-US028565.
XX PR 20-DEC-1999; 99WO-US030095.
XX PR 20-DEC-1999; 99WO-US030999.
XX PR 30-DEC-1999; 99WO-US031274.
XX PR 05-JAN-2000; 2000WO-US000219.
XX PR 06-JAN-2000; 2000WO-US000277.
XX PR 06-JAN-2000; 2000WO-US000376.
XX PR 11-FEB-2000; 2000WO-US003565.
XX PR 18-FEB-2000; 2000WO-US004341.
XX PR 18-FEB-2000; 2000WO-US004342.
XX PR 22-FEB-2000; 2000WO-US004414.
XX (GETH) GENENTECH INC.
XX PA
XX PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
PI Stewart TA, Tamas D, Watanabe CK, Wood WI, Yan M;
XX
XX WPI; 2000-572271/53.
XX DR N-PSDB; AAC58586.
XX
XX Sixty four PEO polypeptides, useful in the diagnosis and treatment of
XX immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
XX arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
XX
XX Claim 33; Fig 16; 309pp; English.

XX The present invention describes sixty four human PRO proteins which can
 CC be used in the treatment of immune related diseases. The human PRO
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
 CC treating and diagnosing immune related disorders. The disorders are
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
 CC immune-mediated renal disease, demyelinating diseases of the central
 CC disease, peripheral nervous systems, hepatobiliary diseases, inflammatory bowel
 CC disease, gluten-sensitive enteropathy and whipple's disease, autoimmune
 CC or immune-mediated skin diseases, allergic diseases, immunological
 CC diseases of the lung, and transplantation associated diseases including
 CC graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
 CC represent PCR primers and hybridisation probes used in the isolation of
 CC human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
 CC represent human PRO polynucleotide and protein sequences given in the
 CC exemplification of the present invention
 XX
 XX Sequence 312 AA;

Query Match 99.2%; Score 385; DB 3; Length 312;
 Best Local Similarity 97.4%; Pred. No. 5.5e-45;
 Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YHKAYGFSAPKDDQVVAVYQEAALACKTPKTKVXSRLWKLGSRVSFVYQOQLQGD 60
 DB 23 YHKAYGFSAPKDDQVVAVYQEAALACKTPKTKVXSRLWKLGSRVSFVYQOQLQGD 82

QY 61 FKNRAEMIDFNIRKN 76
 DB 83 FKNRAEMIDFNIRKN 98

RESULT 12

AAV70668
 ID AAV70668 standard; protein; 312 AA.

XX AC AAY70668;

DT 18-JUL-2000 (first entry)

XX Human PRO245 protein.

XX PRO245; UNQ219; dermatological; immunosuppressive; antiinflammatory;
 KW immunostimulant; antiaesthetic; antirheumatic; antiarthritic; virucide;
 KW antiallergic; haemostatic; hepatotropic; antidiabetic; antianaemic;
 KW nephrotropic; neuroprotective; anticoagulant; immunological disorder;
 KW lung; pneumonia; skin; psoriasis; kidney; glomerulonephritis; arthritis;
 KW spondyloarthritis; SLE; systemic lupus erythematosus; scleroderma;
 KW idiopathic inflammatory myopathy; anaemia; thrombocytopenia; diabetes;
 KW thyroiditis; grave's disease; demyelinating disease; multiple sclerosis;
 KW Crohn's disease; hepatobiliary disease; hepatitis; asthma; human;
 KW graft-versus-host-disease.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 39..43
 FT Modified-site /note="Casein Kinase II phosphorylation site"
 FT Modified-site 59..63
 FT Modified-site /note="Casein Kinase II phosphorylation site"
 FT Modified-site 98..102
 FT Modified-site /note="N-glycosylation site"
 FT Modified-site 100..104
 FT Modified-site /note="Casein Kinase II phosphorylation site"
 FT Modified-site 149..153
 FT Modified-site /note="Casein Kinase II phosphorylation site"
 FT Modified-site 182..188
 FT Modified-site /note="N-myristoylation site"
 FT Modified-site 187..191

FT Modified-site /note="N-glycosylation site"
 FT 205..209
 FT Modified-site /note="Casein Kinase II phosphorylation site"
 FT 226..230
 FT Modified-site /note="Amidation site"
 FT 236..240
 FT Modified-site /note="N-glycosylation site"
 FT 239..245
 FT Modified-site /note="N-myristoylation site"
 FT 255..261
 FT Modified-site /note="N-myristoylation site"
 FT 257..263
 FT Modified-site /note="N-myristoylation site"
 FT 277..281
 FT Modified-site /note="N-glycosylation site"
 FT 284..288
 FT Modified-site /note="Casein Kinase II phosphorylation site"
 FT 305..311
 FT Modified-site /note="N-myristoylation site"
 XX
 XX WO200015797-A2.
 XX
 XX 23-MAR-2000.
 XX
 XX 15-SEP-1999; 99WO-US021547.
 XX
 XX 17-SEP-1998; 98US-0100858P.
 XX 17-SEP-1998; 98WO-US019437.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Fong S, Goddard A, Gurney AL, Tumas D, Wood WI;
 XX
 XX WPI; 2000-271435/23.
 XX N-PSDB; AA252202.
 XX
 XX Composition for treatment and diagnosis of immune related diseases e.g.
 XX Grave's disease comprises a PRO245, PRO217, PRO301, PRO266, PRO335,
 XX PRO331 or PRO326 polypeptide or its agonists or antagonists (preferably
 XX antibodies).

Example 1; Fig 4; 201pp; English.

The present sequence is the human protein PRO245, encoded by UNQ219 cDNA,
 designated as clone DNA35638. It is isolated from human foetal liver
 tissue. It has structural homology to transmembrane protein receptor
 tyrosine kinase family and has 60% amino acid identity with human c-myc
 protein. It enhances or suppresses the infiltration of inflammatory cells
 into tissues, proliferation of T-lymphocytes and modulates the immune
 response. This sequence is useful for treatment of immune related
 disorders, like SLE, rheumatoid/juvenile arthritis, spondyloarthritis,
 systemic sclerosis (scleroderma), idiopathic inflammatory myopathies such
 as dermatomyositis, Sjogren's syndrome, systemic vasculitis, sarcoidosis,
 autoimmune haemolytic anaemia, thrombocytopenia, thyroiditis e.g. Grave's
 disease, diabetes mellitus, immune-mediated renal disease e.g.
 glomerulonephritis, demyelinating diseases such as multiple sclerosis and
 Guillain-Barre syndrome, hepatobiliary diseases like hepatitis and
 primary biliary cirrhosis, inflammatory and fibrotic lung diseases such
 as inflammatory bowel disease (e.g. Crohn's disease), autoimmune or
 immune-mediated skin diseases such as psoriasis, allergies like asthma,
 immunological diseases of the lungs such as eosinophilic pneumonia and
 transplantation associated diseases such as graft-versus-host-disease

Sequence 312 AA;

Query Match 99.2%; Score 385; DB 3; Length 312;

Best Local Similarity 97.4%; Pred. No. 5.5e-45;

Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YHKAYGFSAPKDDQVVAVYQEAALACKTPKTKVXSRLWKLGSRVSFVYQOQLQGD 60

DB 23 YHKAYGFSAPKDDQVVAVYQEAALACKTPKTKVXSRLWKLGSRVSFVYQOQLQGD 82

QY 61 FKRAEMIDFNIRIKN 76
DB 83 FKRAEMIDFNIRIKN 98

RESULT 13
ID AAB24401 standard; protein; 312 AA.
AC AAB24401;
XX
XX
XX 07-NOV-2000 (first entry)
XX Human PRO245 protein sequence SEQ ID NO:67.
XX Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
KW angiogenic; proliferative; cardiac; cardiovascular; antiatherosclerotic;
KW cytostatic; Gene therapy; vaccine.
XX
XX Homo sapiens.
XX
XX WO200032221-A2.
XX
XX
XX 08-JUN-2000.
XX
XX 30-NOV-1999; 99WO-US028313.
XX
XX 01-DEC-1998; 98WO-US025108.
XX 16-DEC-1998; 98US-0112850P.
XX 12-JAN-1999; 99US-0115554P.
XX 08-MAR-1999; 99WO-US005028.
XX 12-MAR-1999; 99US-0123957P.
XX 28-APR-1999; 99US-0131445P.
XX 14-MAY-1999; 99US-0134287P.
XX 02-JUN-1999; 99WO-US012252.
XX 20-JUN-1999; 99US-0141037P.
XX 28-JUL-1999; 99US-0144758P.
XX 01-SEP-1999; 99US-0145698P.
XX 08-SEP-1999; 99WO-US020111.
XX 13-SEP-1999; 99WO-US020594.
XX 15-SEP-1999; 99WO-US021090.
XX 15-SEP-1999; 99WO-US021547.
XX 05-OCT-1999; 99WO-US023089.
XX 23-OCT-1999; 99US-0162506P.
XX
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ;
PI Goddard A, Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF;
PI Smith V, Watanabe CK, Williams PW, Wood WI;
XX
XX WPI; 2000-412154/35.
DR N-PSDB; AAA77562.
XX
XX
XX Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing
PT and treating atherosclerosis, cardiovascular, endothelial or angiogenic
PT disorders in mammals.
XX
XX Claim 72; Fig 28; 315pp; English.
XX
XX The present invention describes nucleic acids encoding PRO polypeptides
CC useful for preventing, diagnosing and treating atherosclerosis, cardiovascular,
CC cardiovascular, endothelial or angiogenic disorder in mammals by
CC modulating cell proliferation, angiogenesis and cardiovascularisation,
CC and for identifying agonists and antagonists of these processes. The
CC nucleic acids and the proteins they encode may be used in the prevention,
CC treatment and diagnosis of diseases associated with inappropriate PRO
CC expression such as cardiovascular, endothelial or angiogenic disorders in
CC mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For
CC example, the nucleic acids (NCs) and vectors containing them and the PRO
CC polypeptide may be used to treat disorders associated with decreased PRO

CC expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent
CC nucleotide and protein sequences used in the exemplification of the
CC present invention
XX
XX SQ Sequence 312 AA;
XX
XX Query Match 99.2%; Score 385; DB 3; Length 312;
XX Best Local Similarity 97.4%; Pred. No. 5.5e-45;
XX Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1 YHKAYGFSAPKDDQVVTAVYQEAILEACKTPKTVKSRLEWKLGRSVFVYQOTLQGD 60
DB 23 YHKAYGFSAPKDDQVVTAVYQEAILEACKTPKTVKSRLEWKLGRSVFVYQOTLQGD 82
QY 61 FKRAEMIDFNIRIKN 76
DB 83 FKRAEMIDFNIRIKN 98
XX
XX
XX RESULT 14
XX ADC78384
XX ID ADC78384 standard; protein; 312 AA.
XX
XX AC ADC78384;
XX
XX 01-JAN-2004 (first entry)
XX Human PRO245 protein.
XX
XX antinflammatory; antiulcer; cytostatic; aniposoriatic; antiparkinsonian;
KW neurotrophic; neuroprotective; vasotropic; chemotactic; angiogenic;
KW antiarteriosclerotic; cardiac; antidiabetic; cerebroprotective;
KW thrombolytic; immunomodulator; enterocolitis; Zollinger-Ellison syndrome;
KW gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease;
KW Alzheimer's; ALS; neuropathy; dermal scarring; wound healing;
KW nerve repair; thrombosis; bone; cartilage formation; angiogenesis;
KW asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder;
KW atherosclerosis; cardiac injury; infertility; premature aging; AIDS;
KW diabetes; stroke; gene therapy; transgenic; PRO; human.
XX
XX Homo sapiens.
XX WO200015796-A2.
XX
XX 23-MAR-2000.
XX
XX 15-SEP-1999; 99WO-US021090.
XX
XX 16-SEP-1998; 98WO-US019330.
XX
XX (GETH) GENENTECH INC.
XX
XX Chen J, Goddard A, Gurney AL, Hillan K, Pennica D, Wood WI;
PI Yuan J;
XX
XX WPI; 2000-271434/23.
DR N-PSDB; ADC78383.
XX
XX Novel nucleic acids encoding secreted and transmembrane polypeptides with
PT homology, e.g. to growth and cancer-associated antigens.
XX
XX Claim 12; SEQ ID NO 64; 355pp; English.
XX
XX The invention relates to a novel nucleic acid encoding a PRO polypeptide.
CC The polypeptides and polynucleotides of the invention may be useful as
CC research tools and as therapeutics for treating enterocolitis, Zollinger-
CC Ellison syndrome, gastrointestinal ulceration, psoriasis, cancer,
CC Parkinson's disease, Alzheimer's disease, ALS, neuropathies, dermal
CC scarring and wound healing, nerve repair, thrombosis, bone and/or
CC cartilage formation, angiogenesis, asthma, rheumatoid arthritis, multiple
CC sclerosis, inflammatory disorders, atherosclerosis, cardiac injury,
CC infertility, premature aging, AIDS, diabetes complications and stroke.

CC The molecules may also be utilised during gene therapy procedures and
CC transgenic animal production. The current sequence is that of the human
CC PRO protein of the invention.
XX
SQ Sequence 312 AA;

Query Match 99.2%; Score 385; DB 3; Length 312;
Best Local Similarity 97.4%; Pred. No. 5.5e-45;
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YHKAYGFSAPKDDQVVTAVYQEAAILACKTPKKTIXSRLEWKKLGRSVFVYQQTQGD 60
DB 23 YHKAYGFSAPKDDQVVTAVYQEAAILACKTPKKTIXSRLEWKKLGRSVFVYQQTQGD 82

QY 61 FKNAEMIDFNIRIKN 76
DB 83 FKNAEMIDFNIRIKN 98

RESULT 15
AAB80222
ID AAB80222 standard; protein; 312 AA.
XX
AC AAB80222;
XX
DT 24-APR-2001 (first entry)
XX
DE Human PRO245 protein.
XX
XX Human; PRO; dermatological; antipsoriatic; cytostatic; antinflammatory;
KW antiparkinsonian nootropic; neuroprotective; vulnery; cardiant;
KW antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;
KW antiarthritic; antiinfertility; antidiabetic; antiviral; diabetes;
KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
KW ischaemia; inflammation.
XX
OS Homo sapiens.
XX
PN WO200104311-A1.
XX
PD 18-JAN-2001.
XX
PF 22-FEB-2000; 2000WO-US000414.
XX
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
XX
PA (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy WA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
XX WPI; 2001-081051/09.
DR N-PSDB; AAF72383.
XX
PT Sixty one nucleic acids encoding PRO polypeptides which are useful in the

PT treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous
PT cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
PT disease).
XX
PS Claim 1; Fig 24; 393pp; English.
XX
XX The present sequence is one of sixty one novel secreted and transmembrane
CC PRO polypeptides. The PRO polypeptides are useful for treating skin
CC diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma),
CC gastrointestinal disorders (e.g. enterocolitis), neurodegenerative
CC diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair,
CC cardiovascular disorders (e.g. endometrial bleeding angiogenesis,
CC ischaemia such as coronary ischaemia, atherosclerosis), inflammatory
CC disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis),
CC infertility, AIDS and diabetes and retinal disorders such as retinitis
CC pigmentosum. The PRO nucleic acids have applications in molecular
CC biology, including use as hybridization probes, and in chromosome and
CC gene mapping
XX
SQ Sequence 312 AA;

Query Match 99.2%; Score 385; DB 4; Length 312;
Best Local Similarity 97.4%; Pred. No. 5.5e-45;
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YHKAYGFSAPKDDQVVTAVYQEAAILACKTPKKTIXSRLEWKKLGRSVFVYQQTQGD 60
DB 23 YHKAYGFSAPKDDQVVTAVYQEAAILACKTPKKTIXSRLEWKKLGRSVFVYQQTQGD 82

QY 61 FKNAEMIDFNIRIKN 76
DB 83 FKNAEMIDFNIRIKN 98

Search completed: July 15, 2004, 23:52:47
Job time : 20.7112 secs

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OM protein - protein search, using sw model

Run on: July 15, 2004, 23:50:59 ; Search time 5.89305 Seconds
(without alignments)
665.797 Million cell updates/sec

Title: US-09-852-797-76_COPY_23_98

Perfect score: 388

Sequence: 1 YHKAYGFSAPKDDQVVTAVX.....LQGFKNRAEMIDFNIRKN 76

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
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3: /cgn2_6/ptodata/2/iaa/6A COMB pep.*
4: /cgn2_6/ptodata/2/iaa/6B COMB pep.*
5: /cgn2_6/ptodata/2/iaa/PTCTUS COMB pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	385	99.2	312	4	US-09-254-465A-9
2	385	99.2	312	4	US-09-907-794A-64
3	385	99.2	312	4	US-09-905-125A-64
4	385	99.2	312	4	US-09-902-775A-64
5	384	99.0	298	4	US-09-152-060-76
6	80	20.6	310	4	US-09-907-794A-423
7	80	20.6	310	4	US-09-905-125A-423
8	80	20.6	310	4	US-09-902-775A-423
9	62.5	16.1	213	4	US-09-107-532A-5581
10	59	15.2	602	1	US-08-428-926-5
11	59	15.2	602	1	US-08-428-927-5
12	59	15.2	602	1	US-08-428-298-5
13	59	15.2	602	1	US-08-339-517-5
14	59	15.2	724	4	US-09-562-737-22
15	58.5	15.1	262	4	US-09-328-352-5407
16	58	14.9	121	4	US-09-107-532A-7107
17	57.5	14.8	602	1	US-08-168-091A-2
18	56.5	14.6	115	3	US-08-483-749A-6
19	56.5	14.6	138	2	US-09-057-762-13
20	56.5	14.6	138	3	US-08-326-119A-13
21	56.5	14.6	1531	4	US-09-576-594-203
22	56	14.4	354	4	US-09-393-627B-28
23	55.5	14.3	196	4	US-09-328-352-4778
24	55.5	14.3	257	4	US-09-543-681A-6195
25	55	14.2	95	4	US-09-328-352-6933
26	55	14.2	125	2	US-08-039-198B-12
27	55	14.2	125	2	US-08-182-067-2

28	55	14.2	125	2	US-08-465-313-2	Sequence 2, Appli
29	55	14.2	125	4	US-09-809-739-1	Sequence 1, Appli
30	55	14.2	437	4	US-09-252-991A-22414	Sequence 22414, A
31	54.5	14.0	96	4	US-09-489-039A-8700	Sequence 8700, Ap
32	54.5	14.0	296	4	US-09-252-991A-26057	Sequence 26057, A
33	54.5	14.0	488	4	US-09-328-352-4396	Sequence 4396, Ap
34	54.5	14.0	926	4	US-09-543-681A-6681	Sequence 6681, Ap
35	54	13.9	30	4	US-08-948-131-3	Sequence 3, Appli
36	54	13.9	47	2	US-08-310-912A-58	Sequence 58, Appli
37	54	13.9	47	3	US-08-841-089-58	Sequence 58, Appli
38	54	13.9	47	3	US-09-301-085-58	Sequence 58, Appli
39	54	13.9	47	5	PCT-US95-04570-58	Sequence 58, Appli
40	54	13.9	579	4	US-09-543-681A-5296	Sequence 5296, Ap
41	54	13.9	670	4	US-09-328-352-6725	Sequence 6725, Ap
42	54	13.9	105	4	US-09-497-997C-25	Sequence 25, Appli
43	53.5	13.8	119	4	US-08-875-674A-1	Sequence 1, Appli
44	53.5	13.8	122	4	US-09-556-877-30	Sequence 30, Appli
45	53.5	13.8				

ALIGNMENTS

RESULT 1
US-09-254-465A-9
; Sequence 9, Application US/09254465A
; Patent No. 6410708
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Napier, Mary A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
; TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
; FILE REFERENCE: P1216R1(US)
; CURRENT APPLICATION NUMBER: US/09/254,465A
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: PCT/US98/24855
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: US 60/066,364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 60/078,936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: PCT/US98/19437
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 30
; SEQ ID NO 9
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-254-465A-9

Query Match	99.2%;	Score 385;	DB 4;	Length 312;
Best Local Similarity	97.4%;	Pred. NO. 2e-44;		
Matches	74;	Conservative 0;	Mismatches 2;	Indels 0; Gaps 0;
QY	1	YHKAYGFSAPKDDQVVTAVX	YQEAIALCKTPKTVXSRLEWKKLGRSVFYVYQQTQGD	60
Db	23	YHKAYGFSAPKDDQVVTAVX	YQEAIALCKTPKTVXSRLEWKKLGRSVFYVYQQTQGD	82
QY	61	FKNRAEMIDFNIRKN	76	
Db	83	FKNRAEMIDFNIRKN	98	

RESULT 2
US-09-907-794A-64
; Sequence 64, Application US/09907794A
; Patent No. 6635468

Best Local Similarity 97.4%; Pred. No. 2e-44; Indels 0; Gaps 0;
Matches 74; Conservative 0; Mismatches 2;

QY 1 YHKAYGFSAPKDDQVTVAVYQAEAILACKTPKTVXSRLEWKLGRSVSFYVYQQTLOGD 60
Db 23 YHKAYGFSAPKDDQVTVAVYQAEAILACKTPKTVXSRLEWKLGRSVSFYVYQQTLOGD 82

QY 61 FKXRAEMIDFNIRIKN 76
Db 83 FKXRAEMIDFNIRIKN 98

RESULT 3
US-09-905-125A-64
; Sequence 64, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US/09/905,125A
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02

GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US/09/907,794A
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-794A-64

Query Match 99.2%; Score 385; DB 4; Length 312;


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RESULT 4
US-90-902-775A-64
Sequence 64, Application US/09902775A
Patent No. 668451
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Beshtein, David
APPLICANT: Detsnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Flivaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Gimaldi, Christopher J.
APPLICANT: Gurney, Aushin L. J.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transferred
TITLE OF INVENTION: Acids Encoding
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/901000
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/000000
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/200000
PRIOR FILING DATE: 1999-09-08

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Query Match          99.2%; Score 385; DB 4; Length 312;
Best Local Similarity 97.4%; Pred.No. 2e-44;
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 YHKAYGFSAPKQQQVTVAVYQEAILACKTPKKTIVXSRLEWKKLGRSVSFYYQQTIGD 60
Db      23 YHKAYGFSAPKQQQVTVAVYQEAILACKTPKKTIVXSRLEWKKLGRSVSFYYQQTIGD 82

Qy      61 FKNRAEMIDFNIRIKN 76
Db      83 FKNRAEMIDFNIRIKN 98

RESULT 5
US-09-152-060-76
; Sequence 76, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P1.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368

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; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 76
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (42)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (58)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-152-060-76

Query Match          99.0%; Score 384; DB 4; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.6e-44;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YKAYGSAPKDDQVAVXVQEAILACKTPKKTIXSRLEWKLGRSVFVYQQTLQGD 60
DB 23 YKAYGSAPKDDQVAVXVQEAILACKTPKKTIXSRLEWKLGRSVFVYQQTLQGD 82

QY 61 FKRAEMIDFNIRKN 76
DB 83 FKRAEMIDFNIRKN 98

RESULT 6
US-09-907-794A-423
; Sequence 423, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Grøttisen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28

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; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-907-794A-423

Query Match          20.6%; Score 80; DB 4; Length 310;
Best Local Similarity 32.0%; Pred. No. 0.0092;
Matches 16; Conservative 13; Mismatches 19; Indels 2; Gaps 2;

QY 21 YQEAIIAC-KTPKKTIXSRLEWKL-GRSVFVYQQTLQGD FKNRAEMI 68
DB 46 FESVELSCIITDSQSDPRIEWKLIQDEQTYTVFDFNKKIQDLAGRAEIL 95

RESULT 7
US-09-905-125A-423
; Sequence 423, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Grøttisen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

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; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-905-125A-423

Query Match          20.6%; Score 80; DB 4; Length 310;
Best Local Similarity 32.0%; Pred. No. 0.0092;
Matches 16; Conservative 13; Mismatches 19; Indels 2; Gaps 2;

QY      21  YQEAIIAC-KTPKKTIVSRLEKKL-GRSVSFVYVYQOTLQGFQKRAEMI 68
       ::  |||  ::  |||  ::  |||  ::  |||  ::  |||  ::  |||  ::
Db      46  FESVLSCIITDSQTSDPRIEWKXIQDEQATYVFFDNKIQGLLAGRAEIL 95

RESULT 8
US-09-902-775A-423
; Sequence 423, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Debnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Oiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Grimaldi, Christopher J.

```

ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02154

COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107.532A
FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 5581:
SEQUENCE CHARACTERISTICS:
LENGTH: 213 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium

FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...213
SEQUENCE DESCRIPTION: SEQ ID NO: 5581:
US-09-107-532A-5581

Query Match 16.1%; Score 62.5; DB 4; Length 213;
Best Local Similarity 32.9%; Pred. No. 1.4;
Matches 25; Conservative 7; Mismatches 19; Indels 25; Gaps 4;

QY 11 KDOQVTVAVXQEAIALACKTPKTVXSRL-EWKK-----LGRSVSVFY 52
DB 131 KNGKVITA--YSE-----KVDKVVADRLAEWKKTNEQKVTYSSQKNSTGTPSDSG 183

QY 53 YQQTLOGDFKNRAEMI 68
DB 184 SQQTITGSEENQASII 199

RESULT 10
US-08-428-926-5
Sequence 5, Application US/08428926
Patent No. 5667780
GENERAL INFORMATION:
APPLICANT: Ho, Wei-Hsien
APPLICANT: Osherooff, Phyllis L.
TITLE OF INVENTION: SENSORY AND MOTOR NEURON DERIVED FACTOR (SMDF)
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,926
FILING DATE: 25-APR-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/339517
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 853D4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 602 amino acids
TYPE: amino acid
TOPOLOGY: linear

US-08-428-926-5

Query Match 15.2%; Score 59; DB 1; Length 602;
Best Local Similarity 26.6%; Pred. No. 16;
Matches 17; Conservative 12; Mismatches 17; Indels 18; Gaps 3;

QY 11 KDOQVTVAVXQEAIALACKTPKTVXSRL-EWKKLGRSVSVFYQQTLOGDFKNRAEMIDF 70
DB 35 KNGEVAVG---OKLVRCETTSYEPALRFKWLKNGKEIT-----KKNRPE----- 76

QY 71 NIRI 74
DB 77 NVKI 80

RESULT 11
US-08-428-927-5
Sequence 5, Application US/08428927
Patent No. 5756456
GENERAL INFORMATION:
APPLICANT: Ho, Wei-Hsien
APPLICANT: Osherooff, Phyllis L.
TITLE OF INVENTION: SENSORY AND MOTOR NEURON DERIVED FACTOR (SMDF)
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,927
FILING DATE: 25-APR-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/339517
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 853D3
TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-428-927-5

Query Match
Best Local Similarity 15.2%; Score 59; DB 1; Length 602;
Matches 17; Conservative 12; Mismatches 17; Indels 18; Gaps 3;

Qy 11 KDOQVTVAVXYQEAAILACKTPKTVXSRLEWKKLGRSVFVYQQTLOGDFKNRAEMIDF 70
Db 35 KNOEAVVG---QKLVLCRTTSEYPAALRFKWLKNGKEIT-----KKNRPE----- 76

Qy 71 NIRI 74
Db 77 NVKI 80

RESULT 12
US-08-428-298-5
; Sequence 5, Application US/08428298
; Patent No. 5763213
; GENERAL INFORMATION:
; APPLICANT: Ho, Wei-Hsien
; APPLICANT: Osherooff, Phyllis L.
; TITLE OF INVENTION: SENSORY AND MOTOR NEURON DERIVED FACTOR (SMDF)
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428,298
; FILING DATE: 25-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 853D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-428-298-5

Query Match
Best Local Similarity 15.2%; Score 59; DB 1; Length 602;
Matches 17; Conservative 12; Mismatches 17; Indels 18; Gaps 3;

Qy 11 KDOQVTVAVXYQEAAILACKTPKTVXSRLEWKKLGRSVFVYQQTLOGDFKNRAEMIDF 70
Db 35 KNOEAVVG---QKLVLCRTTSEYPAALRFKWLKNGKEIT-----KKNRPE----- 76

Qy 71 NIRI 74
Db 77 NVKI 80

RESULT 13
US-08-339-517-5
; Sequence 5, Application US/08339517
; Patent No. 5770567
; GENERAL INFORMATION:
; APPLICANT: Ho, Wei-Hsien
; APPLICANT: Osherooff, Phyllis L.
; TITLE OF INVENTION: SENSORY AND MOTOR NEURON DERIVED FACTOR (SMDF)
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,517
; FILING DATE: 14-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 853
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-339-517-5

Query Match
Best Local Similarity 15.2%; Score 59; DB 1; Length 602;
Matches 17; Conservative 12; Mismatches 17; Indels 18; Gaps 3;

Qy 11 KDOQVTVAVXYQEAAILACKTPKTVXSRLEWKKLGRSVFVYQQTLOGDFKNRAEMIDF 70
Db 35 KNOEAVVG---QKLVLCRTTSEYPAALRFKWLKNGKEIT-----KKNRPE----- 76

Qy 71 NIRI 74
Db 77 NVKI 80

RESULT 14
US-09-562-737-22
; Sequence 22, Application US/09562737
; Patent No. 6428967
; GENERAL INFORMATION:
; APPLICANT: Herz, Joachim
; APPLICANT: Gotthardt, Michael
; TITLE OF INVENTION: LDL Receptor Signaling Pathways
; FILE REFERENCE: US060708
; CURRENT APPLICATION NUMBER: US/09/562,737
; CURRENT FILING DATE: 2000-05-01
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Mon Jul 19 09:51:26 2004

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; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-562-737-22

Query Match          15.2%; Score 59; DB 4; Length 724;
Best Local Similarity 28.8%; Pred. No. 20; Indels 24; Gaps 2;
Matches 17; Conservative 5; Mismatches 13; Indels 24; Gaps 2;

Qy 31 PKTVXSRLEWKKL-----GRSVSFVYQOTLQ-----GDFKRA 65
Db 489 PSKTRVERERSVKARDWGSSWSQGRDSDVLYYETVTQMEVAYARPIILGDTKDRA 547

RESULT 15
US-09-328-352-5407
; Sequence 5407, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5407
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5407

Query Match          15.1%; Score 58.5; DB 4; Length 262;
Best Local Similarity 25.0%; Pred. No. 6.4; Indels 19; Gaps 3;
Matches 19; Conservative 12; Mismatches 26; Indels 19; Gaps 3;

Qy 7 PSAPKQQQWTVAV-----XYQEAILACKTPKKTIV-----XSRLEWKKLG-RS 47
Db 18 PSAPRYNTLIGVLACVNGVLTFTGLFYQQAIAQDYPIQGFVSHHQENINMKISPOK 77

Qy 48 VSFVYQOTLQDPRN 63
Db 78 FQFVYLKATEGGDYKD 93

Search completed: July 15, 2004, 23:55:47
Job time : 6.89305 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2004, 23:54:34 ; Search time 16.4599 Seconds
(without alignments)
1443.181 Million cell updates/sec

Title: US-09-852-797-76_COPY_23_98

Perfect score: 388

Sequence: 1 YHKXGFSAPKQVVTVAX.....LQGFKNRAEMIDNIRKN 76

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Searched: 1285345 seqs, 312560633 residues

Total number of hits satisfying chosen parameters: 1285345

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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13: /cgn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	385	99.2	298	9	US-09-745-763-38
2	385	99.2	298	9	US-09-799-777-30
3	385	99.2	298	14	US-10-139-849-2
4	385	99.2	298	14	US-10-192-791-2
5	385	99.2	298	16	US-10-601-953-889
6	385	99.2	312	9	US-09-909-320-64
7	385	99.2	312	9	US-09-909-088B-64
8	385	99.2	312	9	US-09-905-291A-64
9	385	99.2	312	9	US-09-953-499-9
10	385	99.2	312	9	US-09-902-853-64
11	385	99.2	312	9	US-09-907-824-64
12	385	99.2	312	9	US-09-907-841-64
13	385	99.2	312	10	US-09-904-011-64
14	385	99.2	312	10	US-09-906-742-64
15	385	99.2	312	10	US-09-906-838-64

16	385	99.2	312	10	US-09-907-613-64	Sequence 64, Appl
17	385	99.2	312	10	US-09-907-942-64	Sequence 64, Appl
18	385	99.2	312	10	US-09-904-859-64	Sequence 64, Appl
19	385	99.2	312	10	US-09-909-204-64	Sequence 64, Appl
20	385	99.2	312	10	US-09-904-820-64	Sequence 64, Appl
21	385	99.2	312	10	US-09-904-786-64	Sequence 64, Appl
22	385	99.2	312	10	US-09-906-646-64	Sequence 64, Appl
23	385	99.2	312	10	US-09-906-700-64	Sequence 64, Appl
24	385	99.2	312	10	US-09-903-786-64	Sequence 64, Appl
25	385	99.2	312	10	US-09-902-903-64	Sequence 64, Appl
26	385	99.2	312	10	US-09-903-749A-64	Sequence 64, Appl
27	385	99.2	312	10	US-09-904-119-64	Sequence 64, Appl
28	385	99.2	312	10	US-09-904-856-64	Sequence 64, Appl
29	385	99.2	312	10	US-09-902-736-64	Sequence 64, Appl
30	385	99.2	312	10	US-09-907-794-64	Sequence 64, Appl
31	385	99.2	312	10	US-09-903-943-64	Sequence 64, Appl
32	385	99.2	312	10	US-09-904-462-64	Sequence 64, Appl
33	385	99.2	312	10	US-09-907-925-64	Sequence 64, Appl
34	385	99.2	312	10	US-09-902-892-64	Sequence 64, Appl
35	385	99.2	312	10	US-09-903-520-64	Sequence 64, Appl
36	385	99.2	312	10	US-09-905-056-64	Sequence 64, Appl
37	385	99.2	312	10	US-09-909-064-64	Sequence 64, Appl
38	385	99.2	312	10	US-09-904-553-64	Sequence 64, Appl
39	385	99.2	312	10	US-09-905-381-64	Sequence 64, Appl
40	385	99.2	312	10	US-09-905-088-64	Sequence 64, Appl
41	385	99.2	312	10	US-09-907-575-64	Sequence 64, Appl
42	385	99.2	312	10	US-09-905-075-64	Sequence 64, Appl
43	385	99.2	312	10	US-09-902-759-64	Sequence 64, Appl
44	385	99.2	312	10	US-09-902-634-64	Sequence 64, Appl
45	385	99.2	312	10	US-09-902-713-64	Sequence 64, Appl

ALIGNMENTS

RESULT 1

US-09-745-763-38

; Sequence 38, Application US/09745763

; Patent No. US20020065394A1

; GENERAL INFORMATION:

; APPLICANT: Jacobs, Kenneth

; McCoy, John M.

; Lavalie, Edward R.

; Collins-Racie, Lisa A.

; Evans, Cheryl

; Merberg, David

; Treacy, Maurice

; Spaulding, Vikki

; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES

; NUMBER OF SEQUENCES: 219

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genetics Institute, Inc.

; STREET: 87 CambridgePark Drive

; CITY: Cambridge

; STATE: MA

; COUNTRY: U.S.A.

; ZIP: 02140

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/745,763

; FILING DATE: 18-Jun-2000

; CLASSIFICATION: <UNKNOWN>

; ATTORNEY/AGENT INFORMATION:

; NAME: Sprunger, Suzanne A.

; REGISTRATION NUMBER: 41,323

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 498-8284

; TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-745-763-38

Query Match 99.2%; Score 385; DB 9; Length 298;
Best Local Similarity 97.4%; Pred. No. 9.6e-43;
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 YHKAIGFSAPKDDQVVTAAYVQEAAILACKTPKKTIVSRLEWKLGSRVSFVYQOTLQGD 60
DB 23 YHKAIGFSAPKDDQVVTAAYVQEAAILACKTPKKTIVSRLEWKLGSRVSFVYQOTLQGD 82
QY 61 FKNRAEMIDFNIRIKN 76
DB 83 FKNRAEMIDFNIRIKN 98

RESULT 2

US-09-799-777-30
Sequence 30, Application US/09799777
Patent No. US20020091244A1

GENERAL INFORMATION:

APPLICANT: Lal, Preeti

Hillman, Jennifer L.

Corley, Neil C.

Guegler, Karl J.

Baugh, Mariah

Sather, Susan

Shah, Purvi

TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS

NUMBER OF SEQUENCES: 154

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/799,777

FILING DATE: 06-Mar-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/002,485

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: BILLINGS, LUCY J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0459 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 298 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: DUODNOT2

CLONE: 1704050

SEQUENCE DESCRIPTION: SEQ ID NO: 30 :

US-09-799-777-30

Query Match 99.2%; Score 385; DB 9; Length 298;
Best Local Similarity 97.4%; Pred. No. 9.6e-43;
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YHKAIGFSAPKDDQVVTAAYVQEAAILACKTPKKTIVSRLEWKLGSRVSFVYQOTLQGD 60
DB 23 YHKAIGFSAPKDDQVVTAAYVQEAAILACKTPKKTIVSRLEWKLGSRVSFVYQOTLQGD 82
QY 61 FKNRAEMIDFNIRIKN 76
DB 83 FKNRAEMIDFNIRIKN 98

RESULT 3

US-10-139-849-2

Sequence 2, Application US/10139849

Publication No. US20030079238A1

GENERAL INFORMATION:

APPLICANT: Cunningham, Sonia

Barros, Maria Pia

TITLE OF INVENTION: A POLYNUCLEOTIDE ENCODING A HUMAN

JUNCTIONAL ADHESION PROTEIN (JAM 2)

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Rockey, Milnamow & Katz, Ltd.

STREET: 180 N. Stetson Avenue, 2 Prudential Plaza,

Suite 4700

CITY: Chicago

STATE: IL

COUNTRY: U.S.A.

ZIP: 60601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/139,849

FILING DATE: 07-May-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/643,929

FILING DATE: 23-Aug-2000

ATTORNEY/AGENT INFORMATION:

NAME: Katz, Martin L.

REGISTRATION NUMBER: 25,011

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5400

TELEFAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 298 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-139-849-2

Query Match 99.2%; Score 385; DB 14; Length 298;
Best Local Similarity 97.4%; Pred. No. 9.6e-43;
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YHKAIGFSAPKDDQVVTAAYVQEAAILACKTPKKTIVSRLEWKLGSRVSFVYQOTLQGD 60
DB 23 YHKAIGFSAPKDDQVVTAAYVQEAAILACKTPKKTIVSRLEWKLGSRVSFVYQOTLQGD 82
QY 61 FKNRAEMIDFNIRIKN 76
DB 83 FKNRAEMIDFNIRIKN 98

Query Match 99.2%; Score 385; DB 9; Length 312;
Best Local Similarity 97.4%; Pred. No. 1e-42;

Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 YHKAYGFSAPKDDQVVTAVYQEAAILACKTPKKTIVXSRLEWKKLGRSVSFVYQQTLOGD 60
Db 23 YHKAYGFSAPKDDQVVTAVYQEAAILACKTPKKTIVXSRLEWKKLGRSVSFVYQQTLOGD 82
QY 61 FKRAEMIDFNIRIKN 76
Db 83 FKRAEMIDFNIRIKN 98

RESULT 7

US-09-909-088B-64
; Sequence 64, Application US/09909088B
; Patent No. US20020146709A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,088B
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095

; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-088B-64

Query Match 99.2%; Score 385; DB 9; Length 312;
Best Local Similarity 97.4%; Pred. No. 1e-42;
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YHKAYGFSAPKDDQVVTAVYQEAAILACKTPKKTIVXSRLEWKKLGRSVSFVYQQTLOGD 60
Db 23 YHKAYGFSAPKDDQVVTAVYQEAAILACKTPKKTIVXSRLEWKKLGRSVSFVYQQTLOGD 82
QY 61 FKRAEMIDFNIRIKN 76
Db 83 FKRAEMIDFNIRIKN 98

RESULT 8

US-09-905-291A-64
; Sequence 64, Application US/09905291A
; Patent No. US20020160374A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,291A
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944

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; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-291A-64

Query Match          99.2%; Score 385; DB 9; Length 312;
Best Local Similarity 97.4%; Pred. No. 1e-42;
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YHKAYGFSAPKDDQVVTVAVYQEAAILACKTPKTVKSRLWKLGSRVSFVYVYQQTLOGD 60
Db 23 YHKAYGFSAPKDDQVVTVAVYQEAAILACKTPKTVKSRLWKLGSRVSFVYVYQQTLOGD 82

QY 61 FKNRAEMIDFNIRKN 76
Db 83 FKNRAEMIDFNIRKN 98

RESULT 9
US-09-953-499-9
; Sequence 9, Application US/09953499
; Publication No. US20020182206A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Napier, Mary A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
; TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
; FILE REFERENCE: P1216R1(US)
; CURRENT APPLICATION NUMBER: US/09/953,499
; CURRENT FILING DATE: 2001-09-14
; PRIOR FILING DATE: 2001-09-14
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: PCT/US98/24855
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: US 60/066,364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 60/078,936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: PCT/US98/19437
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 30
; SEQ ID NO 9
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; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-953-499-9

Query Match          99.2%; Score 385; DB 9; Length 312;
Best Local Similarity 97.4%; Pred. No. 1e-42;
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YHKAYGFSAPKDDQVVTVAVYQEAAILACKTPKTVKSRLWKLGSRVSFVYVYQQTLOGD 60
Db 23 YHKAYGFSAPKDDQVVTVAVYQEAAILACKTPKTVKSRLWKLGSRVSFVYVYQQTLOGD 82

QY 61 FKNRAEMIDFNIRKN 76
Db 83 FKNRAEMIDFNIRKN 98

RESULT 10
US-09-902-853-64
; Sequence 64, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,853
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US/09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
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; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-902-853-64

Query Match          99.2%; Score 385; DB 9; Length 312;
Best Local Similarity 97.4%; Pred. No. 1e-42;
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YHKAYGFSAPKDDQVVTAVXYQEAAILACKTPKTVXSRLWKKLGRSVSFVYYQOTLQGD 60
    |||||
Db 23 YHKAYGFSAPKDDQVVTAVEQEAAILACKTPKTVSSRLWKKLGRSVSFVYYQOTLQGD 82
    |||||

QY 61 FKRAEMIDFNIRKN 76
    |||||
Db 83 FKRAEMIDFNIRKN 98
    |||||

RESULT 11
US-09-907-824-64
; Sequence 64, Application US/09907824
; Publication No. US20020197671A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,824
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
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; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-08-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-824-64

Query Match          99.2%; Score 385; DB 9; Length 312;
Best Local Similarity 97.4%; Pred. No. 1e-42;
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YHKAYGFSAPKDDQVVTAVXYQEAAILACKTPKTVXSRLWKKLGRSVSFVYYQOTLQGD 60
    |||||
Db 23 YHKAYGFSAPKDDQVVTAVEQEAAILACKTPKTVSSRLWKKLGRSVSFVYYQOTLQGD 82
    |||||

QY 61 FKRAEMIDFNIRKN 76
    |||||
Db 83 FKRAEMIDFNIRKN 98
    |||||

RESULT 12
US-09-907-841-64
; Sequence 64, Application US/09907841
; Publication No. US20020198366A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
```

APPLICANT: KJlavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,841
CURRENT FILING DATE: 2001-11-20
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-29
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 64
LENGTH: 312
TYPE: PRT
ORGANISM: Homo sapiens
US-09-907-841-64

Query Match
Best Local Similarity 99.2%; Score 385; DB 9; Length 312;
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YHKAYGFSAPKQQVVTAVYQEAAILACKTPKKTVXSRLWKLGSRVSFVYQQTLQGD 60
23 YHKAYGFSAPKQQVVTAVYQEAAILACKTPKKTVSSRLWKLGSRVSFVYQQTLQGD 82

Db 61 FKRAEMIDFNIRIKN 76
83 FKRAEMIDFNIRIKN 98

RESULT 13
US-09-904-011-64
Sequence 64, Application US/09904011
Publication No. US2003003530A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: KJlavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,011
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 64
LENGTH: 312
TYPE: PRT
ORGANISM: Homo Sapien
US-09-904-011-64

Query Match
Best Local Similarity 99.2%; Score 385; DB 10; Length 312;
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YHKAYGFSAPKQQVVTAVYQEAAILACKTPKKTVXSRLWKLGSRVSFVYQQTLQGD 60
23 YHKAYGFSAPKQQVVTAVYQEAAILACKTPKKTVSSRLWKLGSRVSFVYQQTLQGD 82

Db 61 FKRAEMIDFNIRIKN 76
83 FKRAEMIDFNIRIKN 98

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RESULT 14
US-09-906-742-64
; Sequence 64, Application US/09906742
; Publication No. US20030023054A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertitsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,742
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1998-07-26
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1998-08-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1998-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-906-742-64
Query Match 99.2%; Score 385; DB 10; Length 312;
Best Local Similarity 97.4%; Pred.No.1e-42; Indels 0; Gaps 0;
Matches 74; Conservative 0; Mismatches 2;
QY 1 YHKAYGFSAPKDDQVWTVAYXQEQAILACKTPKKTIVXSRLEWKKLGRSVSVVYQQTLOGD 60
DB 23 YHKAYGFSAPKDDQVWTVAYXQEQAILACKTPKKTIVXSRLEWKKLGRSVSVVYQQTLOGD 82
QY 61 FKNRAEMIDFNIRKN 76
DB 83 FKNRAEMIDFNIRKN 98
RESULT 15
US-09-906-838-64
; Sequence 64, Application US/09906838
; Publication No. US20030027143A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertitsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,838
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1998-07-26
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1998-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05

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; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-906-838-64

Query Match          99.2%; Score 385; DS 10; Length 312;
Best Local Similarity 97.4%; Pred.No. 1e-42;
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YHKAYGFSAPKQQVVTAVYQEAAILACKTPKKTVXSRLEWKLGSRVSFVYYQQTLOGD 60
Db 23 YHKAYGFSAPKQQVVTAVYQEAAILACKTPKKTVXSRLEWKLGSRVSFVYYQQTLOGD 82

QY 61 FKRAEMIDFNIRIKN 76
Db 83 FKRAEMIDFNIRIKN 98
```

Search completed: July 16, 2004, 00:03:55
Job time : 16.4599 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2004, 23:49:58 ; Search time 5.6984 Seconds
(without alignments)
1284.844 Million cell updates/sec

Title: US-09-852-797-76_COPY_23_98

Perfect score: 388
Sequence: 1 YKAYGFSAPKQQVTVAVX.....LQSDFKNRAEMIDFNIRKN 76

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_78:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66	17.0	157	PH0201	hypothetical prote
2	64	16.5	760	T28224	ORF MSV063 probabl
3	62	16.0	231	S45089	hypothetical prote
4	60.5	15.6	156	D86704	transcription elon
5	60.5	15.6	188	A16102	phage polarity sup
6	60.5	15.6	246	A43293	holliday junction
7	60.5	15.6	1526	JN0598	DNA topoisomerase
8	60	15.5	124	C97871	hypothetical prote
9	59.5	15.3	346	A96270	ruvB, holliday jun
10	59.5	15.3	346	A93014	Holliday junction
11	59.5	15.3	414	A12823	aminotransferase [
12	59.5	15.3	414	H97601	hypothetical prote
13	59.5	15.3	444	A50645	hypothetical prote
14	59.5	15.3	803	H18339	flagellar function
15	59.5	15.3	1584	T28224	protein P12M16.25
16	59	15.2	433	S26646	transcription fact
17	59	15.2	602	A45769	acetylcholine rece
18	58.5	15.1	301	A16135	C. parvifingers tra
19	58.5	15.1	333	A2084	ABC transporter, p
20	58.5	15.1	534	E84590	hypothetical prote
21	58	14.9	224	T28224	hypothetical prote
22	58	14.9	586	A2065	hypothetical prote
23	58	14.9	949	H97322	DNA/RNA helicase,
24	57.5	14.8	117	HVMS39	IG heavy chain pre
25	57.5	14.8	119	D27889	IG heavy chain V r
26	57.5	14.8	148	G83681	urease accessory p
27	57.5	14.8	323	E82943	probable ABC subst
28	57.5	14.8	623	S46427	botulinum neurotox
29	57.5	14.8	706	F82148	methyl-accepting C

30	57.5	14.8	848	2	C70203	DNA topoisomerase
31	57.5	14.8	1084	2	B64058	hemoglobin-binding
32	57.5	14.8	1526	2	A44456	DNA topoisomerase
33	57.5	14.8	1528	2	US0703	DNA topoisomerase
34	57	14.7	138	1	BGHU2	spermatid transiti
35	57	14.7	300	2	S76881	hypothetical prote
36	57	14.7	321	2	A64173	conserved hypotet
37	57	14.7	599	2	D70104	DNA topoisomerase
38	57	14.7	641	2	T50091	succinate dehydrog
39	57	14.7	868	2	D86349	hypothetical prote
40	57	14.7	1386	2	T00257	hypothetical prote
41	56.5	14.6	218	2	A33136	proline/arginine-r
42	56.5	14.6	976	1	TWMSMD	macrophage colony-
43	56.5	14.6	1530	2	A40493	DNA topoisomerase
44	56	14.4	589	2	I38598	zinc finger protei
45	56	14.4	810	1	S50889	PRK1 protein - yea

ALIGNMENTS

RESULT 1

PH0201
hypothetical protein 157 - Enterococcus faecalis plasmid pAM-beta-1 (fragment)
C:Species: Enterococcus faecalis
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jul-2000
C:Accession: PH0201
R:Swinfild, R.J.; Oultram, J.D.; Thompson, D.E.; Brehm, J.K.; Minton, N.P.
Gene 87, 79-90, 1990

A:Title: Physical characterisation of the replication region of the Streptococcus faecali
A:Reference number: PH0201; MUID:90236302; PMID:2110101

A:Accession: PH0201

A:Molecule type: DNA

A:Residues: 1-157 <SWI>

A:Cross-references: EMBL:X17092; NID:93023041; PIDN:AAC38598.1; PID:G3023042

C:Genetics:

A:Genome: plasmid

C:Keywords: plasmid replication

Query Match 17.0%; Score 66; DB 2; Length 157;
Best Local Similarity 24.4%; Pred. No. 1.3;
Matches 21; Conservative 17; Mismatches 26; Indels 22; Gaps 4;

QY	1	YKAYGFSAPKQQVTVAVXQEAILACKTPKTVXSRLEWKKLGRSVSFVY---QQTLL 57
DB	59	YFLTYFQSEKQNE---NYQSLRTYVSEKVDIS---DWKALGKTLKSVNYVYSGEQTK 110
QY	58	QO-----DFKNRAEMIDFNI 72
DB	111	KGYSVEYLLNVSDNRSKMQKITFEV 136

RESULT 2

T28224
ORF MSV063 probable early transcription factor large subunit homolog VETF-L (vaccinia A71
C:Species: Melanoplus sanguinipes entomopoxvirus

C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000

C:Accession: T28224

R:Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.

J. Virol. 73, 533-552, 1999

A:Title: The genome of Melanoplus sanguinipes entomopoxvirus.

A:Reference number: Z20484; MUID:99102612; PMID:9847359

A:Accession: T28224

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-760 <AFO>

A:Cross-references: EMBL:AF063866; NID:G4049647; PIDN:AAC97622.1; PID:G4049662

C:Genetics:

A>Note: MSV063

Query Match 16.5%; Score 64; DB 2; Length 760;
Best Local Similarity 27.1%; Pred. No. 1.3;
Matches 23; Conservative 10; Mismatches 34; Indels 18; Gaps 3;

QY 10 PKQQVVTAVXQ---EAILACKTPKTKVXSRLEWKLGSRVSFVYQOTLQDGFKNRAE 66
 DB 119 PNDKSLYNIYQIVGAEVFCVTTNKNGSQSLARSNVYSSVYRDYISEIINNIYKNRYA 178
 QY 67 M-----IDFN--IRIKN 76
 DB 179 MKSSIIDAMYSINIDFQDLRLISN 203

RESULT 3
 S45089
 hypotherical protein eta - Streptococcus pyogenes plasmid pDB101
 C/Species: Streptococcus pyogenes
 C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 15-Oct-1999
 C/Accession: S68123; S45089
 R/Ceglowski, P.; Alonso, J.C.
 Gene 145, 33-39, 1994
 A/Title: Gene organization of the Streptococcus pyogenes plasmid pDB101: sequence analysis
 A/Reference number: S68123; MUID:94320784; PMID:8093174
 A/Accession: S68123
 A/Molecule type: DNA
 A/Residues: 1-231 <CE2>
 A/Cross-references: EMBL:X66468; NID:9496500; PIDN:CAA47095.1; PID:S559958
 A/Experimental source: plasmid pDB101
 C/Genetics:
 A/Genome: plasmid pDB101
 A/Start codon: TTG

Query Match 16.0%; Score 62; DB 2; Length 231;
 Best Local Similarity 23.3%; Pred. No. 6.2; Mismatches 26; Indels 22; Gaps 4;
 Matches 20; Conservative 18

QY 1 YKAYGFSAPKQQVVTAVXQAEAILACKTPKTKVXSRLEWKLGSRVSFVY---QOTL 57
 DB 133 YFLTYYFQSEKNGE-----NYQSSLYVSEKVDIS---DMKALGKTLKSNVYVYGEQTK 184
 QY 58 QG-----DFKNRAEMIDFNI 72
 DB 185 KGYSVEYLLNVTVEDRSKQKXITFEV 210

RESULT 4
 D86704
 transcription elongation factor GreA greA [imported] - Lactococcus lactis subsp. lactis
 C/Species: Lactococcus lactis subsp. lactis
 C/Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
 C/Accession: D86704
 R/Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich
 Genome Res. 11, 731-753, 2001
 A/Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s8
 A/Reference number: A86625; MUID:21235186; PMID:11337471
 A/Accession: D86704
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-156 <STO>
 A/Cross-references: GB:AE005176; PID:gn12723539; PIDN:AAK04734.1; GSPDB:GN00146
 A/Experimental source: strain IL1403
 C/Genetics:
 A/Gene: greA
 C/Superfamily: transcription elongation factor greB
 C/Keywords: transcription factor

Query Match 15.6%; Score 60.5; DB 2; Length 156;
 Best Local Similarity 26.1%; Pred. No. 6.2; Mismatches 28; Indels 25; Gaps 4;
 Matches 24; Conservative 15

QY 3 KAYG-----FSAPKQDQ-----VVTAVXQAEAILACKTPKTKVXSRLEWKLG 46
 DB 38 RSYGDLSENSEYEAADKQAEFEGRISTVEMIRVAEIVDNAKIAQDEVA-----LGK 90
 QY 47 SVSFVYQOTLQDGFK--NRAEMIDFNIRKN 76

Db 91 NVTFEVGTDEESYQIVGTAEADPFSGKISN 122

RESULT 5
 AF1062
 phage polarity suppression protein [imported] - Salmonella enterica subsp. enterica serov. typhi
 C/Species: Salmonella enterica subsp. enterica serovar Typhi
 A/Note: this species has also been called Salmonella typhi
 C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C/Accession: AF1062
 R/Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov. typhi
 A/Reference number: AB0502; MUID:21534947; PMID:11677608
 A/Accession: AF1062
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-188 <PAR>
 A/Cross-references: GB:AL513382; PIDN:CAD06947.1; PID:gl6505594; GSPDB:GN00176
 C/Genetics:
 A/Gene: STI4825
 C/Superfamily: phage P4 amber mutation-suppressing protein

Query Match 15.6%; Score 60.5; DB 2; Length 188;
 Best Local Similarity 34.9%; Pred. No. 7.6; Mismatches 22; Conservative 8; Mismatches 26; Indels 7; Gaps 3;
 Matches 22

QY 16 VTAVXQAEAILACKTPKTKVXSRLEWKLGSRVSFVYQOTLQDGFKNRAEMIDF--NI 72
 DB 1 MTTVTIQAFACQTNKNTWLKRAELADLERE---YREQLLAGDEQIPRRMQDLRDNI 56
 QY 73 RIK 75
 DB 57 DVK 59

RESULT 6
 AH3293
 holliday junction DNA helicase ruvB [imported] - Brucella melitensis (strain 16M)
 C/Species: Brucella melitensis
 C/Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
 C/Accession: AH3293
 R/DelVecchio, V.G.; Kaparal, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanova, I.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesec
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A/Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
 A/Reference number: AB3252; PMID:1175668
 A/Accession: AH3293
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-346 <KUR>
 A/Cross-references: GB:AE008917; PIDN:AAU51515.1; PID:gl7982230; GSPDB:GN00190
 A/Experimental source: strain 16M
 C/Genetics:
 A/Gene: BMEI0334
 A/Map position: I
 C/Superfamily: ruvB protein

Query Match 15.6%; Score 60.5; DB 2; Length 346;
 Best Local Similarity 28.3%; Pred. No. 15; Mismatches 29; Indels 3; Gaps 2;
 Matches 17; Conservative 11

QY 4 AYGSAPKD--QQVVTAVXQAEAILACKTPKTKVXSRLEWKLGSRVSFVYQOTLQDGF 61
 DB 284 AAGLSEPRDAIEDIEPYLIQQGFQ--RTPGRVLTAVAMQHLGPAPAEITQQSQYGLF 342

RESULT 7
 JN0598
 DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) - rat

N;Alternate names: DNA topoisomerase II
C;Species: *Rattus norvegicus* (Norway rat)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 16-Jul-1999
C;Accession: J05598; S32012
R;Park, S.H.; Yoon, J.H.; Kwon, Y.D.; Park, S.D.
Biochem. Biophys. Res. Commun. 193, 787-793, 1993
A;Title: Nucleotide sequence analysis of the cDNA for rat DNA topoisomerase II.
A;Reference number: J05598; MUID:93290677; PMID:8390253
A;Accession: J05598
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-1526 <PAR>
A;Cross-references: EMBL:Z19552; NID:G57963; PIDN:CAA79611.1; PID:G57964
A;Experimental source: testis
A;Note: the authors translated the codon GTG for residue 3 as Leu
C;Comment: This enzyme is required for the segregation of circular DNA molecules after r
C;Genetics:
A;Gene: rTOP2
C;Superfamily: eukaryotic type II DNA topoisomerase; phage T4 DNA topoisomerase (ATP-hyd
C;Keywords: ATP; DNA recombination; DNA repair; DNA replication; isomerase
F;689-916/Domain: phage T4 DNA topoisomerase (ATP-hydrolyzing) medium chain homology <T4
Query Match 15.6%; Score 60.5; DB 2; Length 1526;
Best Local Similarity 27.2%; Pred. No. 71;
Matches 22; Conservative 12; Mismatches 22; Indels 25; Gaps 4;
QY 5 YGFSAPKDDQVTVAVYQEAAILACKTPKTVXSRLW-----KKLGRSVSFVY 53
Db 636 FKYSQPED-----DAAISLAFSKQVDDRKELTNFMEDRRQRKLLGLLPEDYLYG 685
QY 54 QQTLL-----QGDPKRAEMIDFN 71
Db 686 QTTMYLTYNDFINK-ELILFS 705
RESULT 8
C97871
hypothetical protein RC1371 [imported] - Rickettsia conorii (strain Malish 7)
C;Species: *Rickettsia conorii*
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001
C;Accession: C97871
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro
Science 293, 2093-2098, 2001
A;Title: Mechanisms of evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:2142074; PMID:11557893
A;Accession: C97871
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-124 <KUR>
A;Cross-references: GB:AE006914; PIDN:AAL03909.1; PID:G15620516; GSPDB:GN00173
C;Genetics:
A;Gene: RC1371
Query Match 15.5%; Score 60; DB 2; Length 124;
Best Local Similarity 31.8%; Pred. No. 5.6;
Matches 21; Conservative 14; Mismatches 23; Indels 8; Gaps 5;
QY 9 APKQD---QVTVAVYQEAAILACKTPKTV-XSRLEWKKLGRSVSFVYQQTLLQGFKNR 64
Db 36 SPKAEPPKWLAKVGY-ERIQEISDPEKSIDRADRNWKRHRSEKWI--QQRMWQ-KUR 91
QY 65 AEMIDF 70
Db 92 NKLTIDY 97
RESULT 9
A96270
ruvB, Holliday junction binding protein, Holliday branch migration protein (AF175525) (1
C;Species: *Agrobacterium tumefaciens*
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C;Accession: A96270
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorllo, B.; Goldman,

A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tum*
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: A96270
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-346 <KUR>
A;Cross-references: GB:AE007870; PIDN:AAK9683.1; PID:G15159589; GSPDB:GN00170
C;Genetics:
A;Gene: AGR L 2225
A;Map position: linear chromosome
C;Superfamily: ruvB protein
Query Match 15.3%; Score 59.5; DB 2; Length 346;
Best Local Similarity 23.8%; Pred. No. 19;
Matches 15; Conservative 15; Mismatches 26; Indels 7; Gaps 3;
QY 4 AYGFSAKPD--QQVTVAVYQEAAILACKTPKTVXSRLWKKLG---RSVSFVYQQTLL 57
Db 285 AAGLSEPRDAIEDIIEPYMIQGGFIQ-RTPRGRILTATAWKHLGLQPPKDLAAQFRLLT 343
QY 58 QGD 60
Db 344 EDD 346
RESULT 10
AF3014
Holliday junction DNA helicase RuvB [imported] - *Agrobacterium tumefaciens* (strain C58, I
C;Species: *Agrobacterium tumefaciens*
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AF3014
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, I
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AF3014
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-346 <KUR>
A;Cross-references: GB:AE008689; PIDN:AAL44532.1; PID:G17742145; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: ruvB
A;Map position: linear chromosome
C;Superfamily: ruvB protein
Query Match 15.3%; Score 59.5; DB 2; Length 346;
Best Local Similarity 23.8%; Pred. No. 19;
Matches 15; Conservative 15; Mismatches 26; Indels 7; Gaps 3;
QY 4 AYGFSAKPD--QQVTVAVYQEAAILACKTPKTVXSRLWKKLG---RSVSFVYQQTLL 57
Db 285 AAGLSEPRDAIEDIIEPYMIQGGFIQ-RTPRGRILTATAWKHLGLQPPKDLAAQFRLLT 343
QY 58 QGD 60
Db 344 EDD 346
RESULT 11
AI2823
aminotransferase [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont)
C;Species: *Agrobacterium tumefaciens*
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AI2823
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell

S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AE0646
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-444 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD08352.1; PID:g16502397; GSPDB:GN00176
C:Genetics:
A:Gene: SYI268

Query Match 15.3%; Score 59.5; DB 2; Length 444;
Best Local Similarity 26.0%; Pred. No. 25;
Matches 26; Conservative 8; Mismatches 31; Indels 35; Gaps 4;

QY 1 YHKAGFGAPKQDVVTA VXYQEA ILACKTKPKTVXSRL----- 39
DB 285 YAQGHYKADLYKLTA YQSRL----TPWATVISRLRYLPENIDLDSTSPYLPLE 340

QY 40 EWKILGRSVFVY-----QQTQG-DPKRAEMID 69
DB 341 EYKRQSDVSMVLYGSL LKYNQOLEQAKDFAERFTLD 380

RESULT 14
H71839
C:Species: Helicobacter pylori (strain J99)
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C:Accession: H71839
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Werberg, D.; Malls, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric patho
A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: H71839
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-803 <ARN>
A:Cross-references: GB:AE001545; GB:AE001439; NID:g4155776; PIDN:AAD06761.1; PID:g4155785
A:Experimental source: strain J99
C:Genetics:
A:Gene: pflA

Query Match 15.3%; Score 59.5; DB 2; Length 803;
Best Local Similarity 34.5%; Pred. No. 48;
Matches 20; Conservative 12; Mismatches 11; Indels 15; Gaps 5;

QY 7 FSAKPKQVVTA VXYQEA ILACKTKPKTVXSLEW-KKILGRSVFVYQQTILQGDPKN 63
DB 574 FASLKEKAQIIAL--NALKAAKTPSE---KLTWLYRLGRN-----YYR---LGDFKN 617

RESULT 15
F96573
protein F12M16.25 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: F96573
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizlar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: F96573
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1584 <STO>
 A;Cross-references: GB:AE005173; NID:g7769860; PIDN:AAF69538.1; GSPDB:GN00141
 C;Genetics:
 A;Gene: F12M16.25
 A;Map position: 1

Query Match 15.3%; Score 59.5; DB 2; Length 1584;
 Best Local Similarity 25.3%; Pred. No. 98;
 Matches 20; Conservative 13; Mismatches 25; Indels 21; Gaps 3;

Qy 9 APKDQOVTVAVXYQEAI-----LACKTPKTVXSLEWKLGSRVSFVYQOTL----- 57
 Db 70 SPKVDNVVILDHHTAIDSLGVS LTC-----KNVTSVLDIERSGATIAFDYFQKLVEES 125

Qy 58 -----QGDFKNRAEMIDF 70
 Db 126 RGSCKENNDFKMRVFVEY 144

Search completed: July 15, 2004, 23:55:08
 Job time : 6.68984 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2004, 23:49:03 ; Search time 3 25134 Seconds

(without alignments)
1217.140 Million cell updates/sec

Title: US-09-852-797-76_COPY_23_98

Perfect score: 388

Sequence: 1 YHKAYGFSAPKQDVVAVX.....LQDFKNRAEMIDFIRIKN 76

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 segs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	385	99.2	298	1	JAM2_HUMAN
2	64	16.5	760	1	ETP2_MOUSE
3	62.5	16.1	346	1	RVVB_RHIME
4	62.5	16.1	500	1	SVE_LACDE
5	60.5	15.6	156	1	GREA_LACLA
6	60.5	15.6	346	1	RVVB_BRUME
7	60.5	15.6	346	1	RVVB_BRUSU
8	60.5	15.6	1526	1	TP2A_RAT
9	60	15.5	1076	1	CARB_BUCBP
10	59.5	15.3	346	1	RVVB_AGRTS
11	59	15.2	602	1	NRG1_CHICK
12	57.5	14.8	117	1	HV59_MOUSE
13	57.5	14.8	346	1	RVVB_RHIE
14	57.5	14.8	470	1	YPC2_CAEEL
15	57.5	14.8	623	1	HA70_CLOBO
16	57.5	14.8	848	1	TOP1_BORBU
17	57.5	14.8	1066	1	HGBC_HABIN
18	57.5	14.8	1067	1	HGBC_HABIN
19	57.5	14.8	1084	1	HGBC_HABIN
20	57.5	14.8	1526	1	TP2A_CRIGR
21	57.5	14.8	1528	1	TP2A_MOUSE
22	57	14.7	138	1	STP2_HUMAN
23	57	14.7	313	1	ISPE_HABIN
24	57	14.7	599	1	PARE_BORBU
25	57	14.7	641	1	DHSA_SCHPO
26	56.5	14.6	1531	1	TP2A_HUMAN
27	56.5	14.6	1533	1	TP2A_PIG
28	56	14.4	589	1	2132_HUMAN
29	56	14.4	810	1	KIJ5_YEAST
30	55.5	14.3	506	1	SHS1_BOVIN
31	55.5	14.3	551	1	CHIT_NPVAC
32	55.5	14.3	1323	1	ADRA_YEAST
33	55	14.2	79	1	CKS2_XENLA

34	55	14.2	208	1	P1MT_VIBCH
35	55	14.2	704	1	GYS2_YEAST
36	54.5	14.0	571	1	DCP1_SCHPO
37	54.5	14.0	622	1	YXDM_BAGSU
38	54.5	14.0	978	1	KEMS_RAT
39	54	13.9	370	1	MAIK_MARO
40	54	13.9	606	1	VEI_HPV7
41	54	13.9	677	1	UBF1_XENLA
42	54	13.9	1900	1	STT4_YEAST
43	53.5	13.8	121	1	RS13_BACHD
44	53.5	13.8	122	1	RS13_CHLPN
45	53.5	13.8	236	1	TRAR_RHISN

ALIGNMENTS

RESULT 1					
JAM2_HUMAN					
ID	JAM2_HUMAN	STANDARD;	PRT;	298 AA.	
AC	P57087;				
DT	16-OCT-2001 (Rel. 40, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	10-OCT-2003 (Rel. 42, Last annotation update)				
DE	Junctional adhesion molecule 2 precursor (Vascular endothelial				
DE	Junctional adhesion molecule)				
GN	JAM2 OR VEJAM OR C21ORP43.				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Vascular endothelial cells;				
RX	MEDLINE=20317114; PubMed=10779521;				
RA	Palmeri D., van Zante A., Huang C.C., Hemmerich S., Rosen S.D.;				
RT	"Vascular endothelial junction-associated molecule, a novel member of				
RT	the immunoglobulin superfamily, is localized to intercellular				
RT	boundaries of endothelial cells."				
RL	J. Biol. Chem. 275:19139-19145(2000).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Placenta;				
RX	MEDLINE=20507930; PubMed=10945976;				
RA	Cunningham S.A., Arrate M.P., Rodriguez J.M., Bjerkke R.J.,				
RT	"A novel protein with homology to the junctional adhesion molecule:				
RT	Characterization of leukocyte interactions."				
RL	J. Biol. Chem. 275:34750-34756(2000).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Lung;				
RX	MEDLINE=22388257; PubMed=12477932;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Raha S.S., Loquellano N.A., Peters G.J., Carninci P., Prange C.,				
RA	Rosak S.A., McEwan P.J., McKernan K.G., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				
RA	Villalón D.L., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,				
RA	Whiting M., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,				
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,				
RA	Schmurch A., Schein J.E., Jones S.J.M., Marra M.A.;				
RT	"Generation and initial analysis of more than 15,000 full-length				
RT	human and mouse cDNA sequences."				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).				

Q9ku18	vibrio chol
P27472	saccharomyc
Q09737	schizosacch
P42424	bacillus su
Q00495	rattus norv
P12174	marchantia
O40619	human papil
P25979	xenopus lae
P37297	saccharomyc
O50632	bacillus ha
Q92766	chlamydia p
P55407	rhizobium s

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CC -!- FUNCTION: MAY PLAY A ROLE IN THE PROCESSES OF LYMPHOCTYCE HOMING TO
CC SECONDARY LYMPHOID ORGANS.
CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: PROMINENTLY EXPRESSED ON HIGH ENDOTHELIAL
CC VENULES BUT IS ALSO PRESENT ON THE ENDOTHELIA OF OTHER VESSELS.
CC LOCALIZED TO THE INTERCELLULAR BOUNDARIES OF HIGH ENDOTHELIAL
CC CELLS.
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -!- DATABASE: NAME=PROV; NOTE=PROV 2.1-3 (2001);
CC WWW="http://www.ncbi.nlm.nih.gov/prov/1652492186.g.htm".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF255910; AAF81223.1; -.
CC EMBL: AY016009; AAG49022.1; -.
CC EMBL: BC017779; AAH17779.1; -.
CC Genbank: HGNC:14686; JAM2.
CC MIM: 606870; -.
CC GO: GO:0005887; C: integral to plasma membrane; NAS.
CC GO: GO:0016337; P: cell-cell adhesion; NAS.
CC InterPro: IPR007110; Ig-like.
CC InterPro: IPR003598; Ig_C2.
CC Pfam: PF00047; Ig_2.
CC SMART: SM00408; IGC2; 1.
CC PROSITE: PS00835; IG-LIKE; 2.
CC Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.
CC SIGNAL 1 20
CC CHAIN 21 298
CC DOMAIN 21 238
CC DOMAIN 21 238
CC TRANSMEM 239 259
CC DOMAIN 260 298
CC DOMAIN 32 127
CC DOMAIN 134 238
CC DISULFID 50 109
CC DISULFID 155 214
CC CARBOHYD 98 98
CC CARBOHYD 187 187
CC CARBOHYD 236 236
CC SEQUENCE 298 AA; 33207 MW; CA7BE518E22DCAEE CRC64;
CC -----
Query Match 99.2%; Score 385; DB 1; Length 298;
Best Local Similarity 97.4%; Pred. No. 5.3e-40;
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 YHKAIGSAPKDDQVTVAYQYQAILACKTPKTVKSLRWKLGSRVSFVYQOTLQGD 60
Db 23 YHKAIGSAPKDDQVTVAYQYQAILACKTPKTVKSLRWKLGSRVSFVYQOTLQGD 82
Qy 61 FKNRAEMIDFNIRKN 76
Db 83 FKNRAEMIDFNIRKN 98
RESULT 2
EF2_MSEPV STANDARD; PRT; 760 AA.
AC EF2_MSEPV
ID EF2_MSEPV
RA 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Early transcription factor 82 kDa subunit (VF7F large subunit).
GN MSV063.
OS Melanoplus sanguinipes entomopoxvirus (MSEPV).
CC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
CC Entomopoxvirus B.

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OX NCBI_TaxID=83191;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Tucson;
RX MEDLINE=99102612; PubMed=9847359;
RA Alfonso C.L., Tulman E.R., Lu Z., Oma E., Kutish G.F., Rock D.L.;
RT "The genome of Melanoplus sanguinipes entomopoxvirus.";
RL J. Virol. 73:533-552(1999).
CC -!- FUNCTION: ACTS WITH RNA POLYMERASE TO INITIATE TRANSCRIPTION FROM
CC EARLY GENE PROMOTERS. A DNA-DEPENDENT ATPASE ACTIVITY IS
CC ASSOCIATED WITH VTF.
CC -!- SUBUNIT: HETERODIMER OF A 70 kDa AND A 82 kDa SUBUNIT.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF063866; AAC97622.1; -.
CC PIR: T28224; T28224. Pox_VERT_large.
CC InterPro: IPR007532; Pox_VERT_large; 1.
CC Pfam: PF04441; Pox_VERT_large; 1.
CC KW Transcription regulation; Activator.
CC SEQUENCE 760 AA; 89243 MW; 2286DF5A59A3D98 CRC64;
CC -----
Query Match 16.5%; Score 64; DB 1; Length 760;
Best Local Similarity 27.1%; Pred. No. 5.3;
Matches 23; Conservative 10; Mismatches 34; Indels 18; Gaps 3;
Qy 10 PKDQVTVAYQYQ---EAILACKTPKTVKSLRWKLGSRVSFVYQOTLQGD 66
Db 119 PNDKSGILNYIQYIVGAVFCVTKNIGSQLARSNVYSSVYRDYISEINNIYKNRYA 178
Qy 67 M-----IDFN--IRKN 76
Db 179 MKSSIIDAMEYSINIDFQDLRLIN 203
RESULT 3
RUVB_RHIME STANDARD; PRT; 346 AA.
ID RUVB_RHIME
AC Q92M92;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Hollday junction DNA helicase RUVB.
GN RUVB OR R02749 OR SMC03965.
OS Rhizobium meliloti (Sinorhizobium meliloti).
CC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
CC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Gohrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
CC -!- FUNCTION: The ruva-ruvb complex in the presence of ATP renatures
CC cruciform structure in supercoiled DNA with palindromic sequence,
CC indicating that it may promote strand exchange reactions in
CC homologous recombination. RuvAB is an helicase that mediates the
CC Holliday junction migration by localized denaturation and
CC reannealing (By similarity).
CC -!- SUBUNIT: Forms a complex with ruva (By similarity).

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DR HSSP; P27000; IGLN.
DR HAMAP; MF_00022; -.
DR InterPro; IPRO04527; Gltx bact.
DR InterPro; IPRO00924; Glu tRNA-synt 1c.
DR InterPro; IPRO08925; tRNA-synt_bind.
DR InterPro; IPRO01412; tRNA-synt_i.
DR Pfam; PF00749; tRNA-synt_ic; i.
DR PRINTS; TIGR0987; TRNASYNTHGU.
DR TIGRFAMs; TIGR00464; gltX_bact; i.
DR PROSITE; PS00178; AA tRNA_LIGASE I; 1.
KW Aminocyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT SITE 12 22 "HIGH" REGION.
FT SITE 259 263 "KMSKS" REGION.
FT BINDING 262 262 ATP (BY SIMILARITY).
SQ SEQUENCE 500 AA; 56944 MW; 30EAA09133AE6841 CRC64;

Query Match          16.1%; Score 62.5; DB 1; Length 500;
Best Local Similarity   22.1%; Pred. No. 5.1;
Matches    15; Conservative      12; Mismatches     22; Indels       19; Gaps        1

QY           2 HKAYGFSAP-----KDQQVTVAVYQEALLACKTKPKTKVSLEWK 42
Db            :|::|||:         ::||:               |
Dbb           235 YEALGWEPVFGRHMTLIINSATGKKLSKRDESVLQIEQRVELYSQCXPCTSSSLLGWS 294

QY           43 KLGRSVSF 50
Db            :||             .|.
Dbb           295 PVGESEIF 302

RESULT 5
GRETA LACLA
ID GRETA LACLA STANDARD; PRT; 156 AA.
AC Q3CHT2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transcription elongation factor greA (transcript cleavage factor
DE greA).
DE GRE A OR LL0636
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacilliales; Streptococcaceae; Lactococcus.
OX NCBI_TaxId=1360;
RN [1]
RP RP RPP SEQUENCE FROM N.A.
RC STRAIN=ILL1403;
RX MEDLINE=21335186; PubMed=11337471;
RA Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
RA Weissenbach J., Enrich F.S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RL lactis ssp. lactis ILL1403.";
RL Genome Res. 11:731-753(2001).
CC -I- FUNCTION: Necessary for efficient RNA polymerase transcription
CC elongation past template-encoded arresting sites. The arresting
CC sites in DNA have the property of trapping a certain fraction of
CC elongating RNA polymerases that pass through, resulting in locked
CC ternary complexes. Cleavages of the nascent transcript by cleavage
CC factors such as GreA or GreB allows the resumption of elongation
CC from the new 3' terminus. GreA releases sequences of 2 to 3
CC nucleotides (By similarity).
CC -I- SIMILARITY: Belongs to the greA/greB family.
CC -----
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CC -----
CC EMBL; AE006296; AAA04734.1; -.
CC PIR; D86704; D86704.
CC HSSP; P21346; ICRJ.
CC HAMAP; MF_00105; -.
CC DR
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DR InterPro: IPR006359; GreA.
DR InterPro: IPR001437; GreA_GreB.
DR Pfam: PF01272; GreA_GreB_1.
DR Pfam: PF03449; GreA_GreB_N_1.
DR ProDom: PD004918; GreA_GreB_1.
DR TIGRFAMs: TIGR01462; GreA; 1.
DR PROSITE: PS00829; GreA_1; 1.
DR PROSITE: PS00830; GreA_2; FALSE_NEG.
KW Transcription regulation; DNA-binding; Coiled coil; Complete proteome.
FT DOMAIN 8 27 COILED COIL (POTENTIAL).
SQ SEQUENCE 156 AA; 17274 MW; 8558B8E3E02D4C88 CRC64;

Query Match 15.6%; Score 60.5; DB 1; Length 156;
Best Local Similarity 26.1%; Pred. No. 2.5;
Matches 24; Conservative 15; Mismatches 28; Indels 25; Gaps 4;

QY 3 KAYG-----FSAPKDDQ-----VVTAVYQEAIIACKTPKTKTVXSRLEWKKLGR 46
Db RSYGDLSENSEYEAAKDEQAFIEGRISTVETMIRYAEIVDNAKIDKDEVA-----LGK 90

QY 47 SVSFVYVYQTLQGDFK--NRAEMIDFNIRIKN 76
Db NVTFEVGETDEESYQIVGTAEADPFSGKISN 122

RESULT 6
RUVB_BRUME STANDARD; PRT; 346 AA.
AC Q8VIV5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Holliday junction DNA helicase ruvb.
GN RUVB OR BWEI0334.
OS Brucella melitensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / Biotype 1;
RX MEDLINE=20020109; PubMed=11756688;
RA DelVecchio V.G., Kapral R.J., Redkar R.J., Patra G., Mijer C., Los T.,
RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldsman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyripides N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
CC -!- FUNCTION: The ruva-ruvb complex in the presence of ATP renatures
CC cruciform structure in supercoiled DNA with palindromic sequence,
CC indicating that it may promote strand exchange reactions in
CC homologous recombination. RuvAB is an helicase that mediates the
CC Holliday junction migration by localized denaturation and
CC reannealing (By similarity).
CC -!- SUBUNIT: Forms a complex with ruvA (By similarity).
CC -!- SIMILARITY: Belongs to the ruvb family.
CC
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CC
CC EMBL; AE009475; AAL51515.1; -
CC HAVAP; MF 00016; -; 1.
CC InterPro: IPR003593; AAA_ATPase.
CC InterPro: IPR003593; AAA_ATPase_cent.
CC InterPro: IPR004605; RuvB.
CC InterPro: IPR00823; RuvB_C.
CC InterPro: IPR00824; RuvB_N.
CC Pfam; PF00004; AAA; 1.

DR InterPro: IPR008823; RuvB_C.
DR InterPro: IPR008824; RuvB_N.
DR Pfam; PF00004; AAA; 1.
DR Pfam; PF05491; RuvB_C; 1.
DR Pfam; PF05496; RuvB_N; 1.
DR SMART; SM00382; AAA; 1.
DR TIGRFAMs: TIGR00635; ruvb; 1.
KW DNA repair; SOS response; ATP-binding; DNA recombination; Helicase;
FT NP_BIND 59 66 ATP (POTENTIAL).
SQ SEQUENCE 346 AA; 38268 MW; F97710688F919FBC CRC64;

Query Match 15.6%; Score 60.5; DB 1; Length 346;
Best Local Similarity 28.3%; Pred. No. 6;
Matches 17; Conservative 11; Mismatches 29; Indels 3; Gaps 2;

QY 4 AYGFGAPKD--QQVTVAVYQEAIIACKTPKTKTVXSRLEWKKLGRSVFVYVYQTLQGD 61
Db AAGLSEPRDAIEDIEPIYLIQGFQ-RTPGRVLTAVAWCHLGPAPAEIIQSQYGLF 342

RESULT 7
RUVB_BRUSU STANDARD; PRT; 346 AA.
AC Q8FZ02;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Holliday junction DNA helicase ruvb.
GN RUVB OR BR1702.
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29461;
RN SEQUENCE FROM N.A.
RP STRAIN=1330 / Biovar 1;
RX MEDLINE=22247741; PubMed=122711122;
RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
RA Read T.D., Dodson R.J., Umayan L., Brinkac L.M., Beanan M.J.,
RA Nelson W.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
RA Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,
RA Hoover D.L., Lindler L.E., Helling S.M., Boyle S.M., Fraser C.M.;
RT "The Brucella suis genome reveals fundamental similarities between
RT animal and plant pathogens and symbionts.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
CC -!- FUNCTION: The ruva-ruvb complex in the presence of ATP renatures
CC cruciform structure in supercoiled DNA with palindromic sequence,
CC indicating that it may promote strand exchange reactions in
CC homologous recombination. RuvAB is an helicase that mediates the
CC Holliday junction migration by localized denaturation and
CC reannealing (By similarity).
CC -!- SUBUNIT: Forms a complex with ruvA (By similarity).
CC -!- SIMILARITY: Belongs to the ruvb family.
CC
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CC
CC EMBL; AE014463; AAN30602.1; -
CC TIGR; BR1702; -
CC HAVAP; MF 00016; -; 1.
CC InterPro: IPR003593; AAA_ATPase.
CC InterPro: IPR003593; AAA_ATPase_cent.
CC InterPro: IPR004605; RuvB.
CC InterPro: IPR00823; RuvB_C.
CC InterPro: IPR00824; RuvB_N.
CC Pfam; PF00004; AAA; 1.

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DR Pfam; PF05491; RuvB_C; 1.
DR Pfam; PF05496; RuvB_N; 1.
DR SMART; SM00382; AAA; 1.
DR TIGRFAMs; TIGR00635; ruvB; 1.
KW DNA repair; SOS response; ATP-binding; DNA recombination; Helicase;
KW Complete Proteome. 56 ATP (POTENTIAL).
FT NP_BIND 59 38240 MW; E6671088908197AC CRC64;
SQ SEQUENCE 346 AA; 38240 MW; E6671088908197AC CRC64;

Query Match 15.6%; Score 60.5; DB 1; Length 346;
Best Local Similarity 28.3%; Pred. No. 6;
Matches 17; Conservative 11; Mismatches 29; Indels 3; Gaps 2;

QY 4 AYGFSPKQD---QVVTAAYVQEAAILACKTPKTVXSRLEWKKLGRSVSVFYVQOTLQGDF 61
DB 284 AAGLSEPRDAIEDIIBFYLIQGGFLO-RTPGRVLTAVAWQHLGPPAPAEIIQQSQYGLF 342

RESULT 8
TP2A-RAT
ID TP2A-RAT STANDARD; PRT; 1526 AA.
AC P41516;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE DNA topoisomerase II, alpha isozyme (EC 5.99.1.3).
GN TP2A OR TOP2 OR TOP-2
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Testis;
RX MEDLINE=3290677; PubMed=8390253; Park S.D.;
RA Park S.H.; Yoon J.H.; Kwon Y.D.; Park S.D.;
RT "Nucleotide sequence analysis of the cDNA for rat DNA topoisomerase II."
RL Blochm. Biophys. Res. Commun. 193:787-793(1993).
CC -!- FUNCTION: Control of topological states of DNA by transient breakage and subsequent rejoining of DNA strands. Topoisomerase II makes double-strand breaks.
CC -!- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining of double-stranded DNA.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- MISCELLANEOUS: Eukaryotic topoisomerase I and II can relax both negative and positive supercoils, whereas prokaryotic enzymes relax only negative supercoils.
CC -!- SIMILARITY: Belongs to the type II topoisomerase family.

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EMBL; Z46372; CAA86496.1; -
EMBL; Z19552; CAA79611.1; -
EMBL; Z29676; -; NOT_ANNOTATED_CDS.
DR HSSP; P06786; 1BGW.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR003957; CBFA_NFYB_topis.
DR InterPro; IPR001241; DNA_topoisomII.
DR InterPro; IPR002205; DNA_topoisolv.
DR Pfam; PF00204; DNA_gyraseB; 1.
DR Pfam; PF00521; DNA_topoisolv; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR PRINTS; PR00615; COAATSUBUNTA.
DR PRINTS; PR00418; TP12FAMILY.
DR ProDom; PD000742; DNA_topoisolv; 1.

DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00433; TOP2c; 1.
DR SMART; SM00434; TOP4c; 1.
DR PROSITE; PS00177; TOPOISOMERASE_II; 1.
KW isomerase; Topoisomerase; DNA-binding; ATP-binding; Nuclear protein.
KW NP_BIND 159 164 ATP (POTENTIAL).
FT ACT_SITE 803 803 DNA_CLEAVAGE (BY SIMILARITY).
SQ SEQUENCE 1526 AA; 173220 MW; A1961ABDB1B050F CRC64;

Query Match 15.6%; Score 60.5; DB 1; Length 1526;
Best Local Similarity 27.2%; Pred. No. 30;
Matches 22; Conservative 12; Mismatches 22; Indels 25; Gaps 4;

QY 5 YGFSAPKQDQVVTAAYVQEAAILACKTPKTVXSRLEW-----KKLGRSVSVFYV 53
DB 636 FKYSQPD-----DAAISLAFSKQVDDRKWLTFNFMEDRRQRKLGLEDYLYG 685

QY 54 QOTL---QGDFKNRAEMIDFN 71
DB 686 QTTMYLTYNDFINK-ELILFS 705

RESULT 9
CARB_BUCBP
ID CARB_BUCBP STANDARD; PRT; 1076 AA.
AC P59448;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
GN CARB OR BBP134.
OS Buchnera aphidicola (subsp. Baizhongia pistaciae).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OX Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=135842;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426501; PubMed=12522265;
RA Van Ham R.C.H.J.; Kamerbeek J.; Palacios C.; Rausell C.; Abascal F.; Bastolla U.; Fernandez J.M.; Jimenez I.; Postigo M.; Silva F.J.; Tamames J.; Viguera E.; Latorre A.; Valencia A.; Moran F.; Moya A.; "Reductive genome evolution in Buchnera aphidicola."
RT Proc. Natl. Acad. Sci. U.S.A. 100:581-586(2003).
RL -!- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + phosphate + L-glutamate + carbamoyl phosphate.
CC -!- COFACTOR: Binds 3 manganese ions per subunit (By similarity).
CC -!- PATHWAY: Arginine biosynthesis.
CC -!- PATHWAY: Pyrimidine biosynthesis.
CC -!- SUBUNIT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By similarity).
CC -!- SIMILARITY: Belongs to the carb family.

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EMBL; AB014016; AAO26868.1; -
DR HAMAP; MF_01210; -; 1.
DR InterPro; IPR006275; Cara_L_glu.
DR InterPro; IPR005483; CPase_L.
DR InterPro; IPR005479; CPase_L_D2.
DR InterPro; IPR005480; CPase_L_D3.
DR InterPro; IPR005481; CPase_L_N.
DR InterPro; IPR004362; MGS-like.
DR Pfam; PF00289; CPase_L_Chain; 2.
DR Pfam; PF02786; CPase_L_D2; 2.

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DR Pfam; PF02787; CPSase_L_D3; 1.
DR Pfam; PF02142; MGS; 1;
DR PRINTS; PRO0098; CPSASE
DR TIGRFAMs; TIGR01369; CPSaseII_lrg; 1.
DR PROSITE; PS00866; CPSASE_1; FALSE_NEG.
DR PROSITE; PS00867; CPSASE_2; 2.
KW Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
KW ATP-binding; Manganese; Complete proteome.
FT DOMAIN 1 403 CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
FT DOMAIN 404 553 OLIGOMERIZATION DOMAIN.
FT DOMAIN 554 936 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
FT DOMAIN 937 1076 ALLOSTERIC DOMAIN.
FT REPEAT 1 553
FT REPEAT 554 1076
FT NP_BIND 153 210
FT NP_BIND 303 354
FT METAL 285
FT METAL 286
FT METAL 289
FT METAL 301
FT METAL 301
FT METAL 829
FT METAL 841
SQ SEQUENCE 1076 AA; 120059 MW; 37PAF26E11AFEC03 CRC64;

Query Match 15.5%; Score 60; DB 1; Length 1076;
Best Local Similarity 30.2%; Pred. No. 24;
Matches 16; Conservative 9; Mismatches 28; Indels 0; Gaps 0;

QY 11 KQQVVTAVXYQEAILACKTPKTVXSRLEWKLGRSVFVYQOQTQGDFFKN 63
Db 688 KQPKNATVTNI-QEAILQAKSIKYPIIMIRPSVVGQSWEIVYDEKNTNFNN 740

RESULT 10
RUB AGRT5
ID RUVB AGRT5 STANDARD; PRT; 346 AA.
AC Q8U9K6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Holliday junction DNA helicase ruvb.
GN RUVB OR AFU3722 OR AGR L. 2225.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Boeve D.Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphammachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58."
RL Science 294:2317-2323(2001).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houniel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Woliam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub G.,
RA Clelo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58."
RL Science 294:2323-2328(2001).

CC -!- FUNCTION: The ruvA-ruvB complex in the presence of ATP renatures
CC cruciform structure in supercoiled DNA with palindromic sequence,
CC indicating that it may promote strand exchange reactions in
CC homologous recombination. RuvAB is an helicase that mediates the
CC Holliday junction migration by localized denaturation and
CC reannealing (By similarity).
CC -!- SUBUNIT: Forms a complex with ruvA (By similarity).
CC -!- SIMILARITY: Belongs to the ruvB family.
CC
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CC
CC EMBL; AR009303; AAL44532.1; -.
CC EMBL; AR008311; AAK89683.1; -.
CC PIR; A96270; A96270.
CC PIR; AF3014; AF3014.
CC HAMAP; MF_00016; 1.
CC InterPro; IPR003593; AAA_ATPase.
CC InterPro; IPR003959; AAA_ATPase_cent.
CC InterPro; IPR004605; RuvB.
CC InterPro; IPR008823; RuvB_C.
CC InterPro; IPR008824; RuvB_N.
CC Pfam; PF00004; AAA; 1.
CC Pfam; PF05491; RuvB_C; 1.
CC Pfam; PF05496; RuvB_N; 1.
CC SMART; SM00382; AAA; 1.
CC TIGRFAMs; TIGR00635; ruvB; 1.
CC DNA repair; SOS response; ATP-binding; DNA recombination; Helicase;
CC Complete proteome.
CC NP_BIND 60 67 ATP (POTENTIAL).
CC SEQUENCE 346 AA; 38118 MW; 002E618EA234A189 CRC64;

Query Match 15.3%; Score 59.5; DB 1; Length 346;
Best Local Similarity 23.8%; Pred. No. 8;
Matches 15; Conservative 15; Mismatches 26; Indels 7; Gaps 3;

QY 4 AVGESAPKD--QQVVTAVXYQEAILACKTPKTVXSRLEWKLKG----RSVSFVYQOQL 57
Db 285 AAGLSEPRDALEIDIEPIWIOGFIQ-RTPRGRILTATAWKHLGLQPPKDLEAAQFRLL 343

QY 58 QGD 60
Db 344 EDD 346

RESULT 11
NRGI_CHICK
ID NRGI_CHICK STANDARD; PRT; 602 AA.
AC Q05199; O73750; O73751; O73752;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Pro-neuregulin-1 precursor (Pro-NRGI) [Contains: Neuregulin-1
DE (Acetylcholine receptor inducing activity) (ARIA)].
OS NRGI OR ARIA.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE.
RX STRAIN=white leghorn; TISSUE=Brain;
RX MEDLINE=93201602; PubMed=8453670;
RX Falls D.L., Rosen K.M., Corfas G., Lane W.S., Fischbach G.D.;
RT "ARIA, a protein that stimulates acetylcholine receptor synthesis, is
RT a member of the neu ligand family."
RL Cell 72:801-815(1993).

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[2] SEQUENCE FROM N.A. (ISOFORMS 2; 3 AND 4).
RP TISSUE=Brain, and Spinal cord;
RC MEDLINE=98150951; PubMed=9491987;
RX Yang X., Kuo Y., Devay P., Yu C., Role L.;
RT "A cysteine-rich isoform of neu-regulin controls the level of
RT expression of neuronal nicotinic receptor channels during
RT synaptogenesis.";
RL Neuron 20:235-270(1998).
CC -1- FUNCTION: Direct ligand for the ERBB tyrosine kinase receptors.
CC The multiple isoforms perform diverse functions: Cysteine-rich
CC domain containing isoforms (isoforms 2-4) probably regulate the
CC expression of nicotinic acetylcholine receptors at developing
CC interneuronal synapses. The Ig-NRG isoform is required for the
CC initial induction and/or maintenance of the mature levels of
CC nicotinic receptors at neuromuscular synapses.
CC -1- SUBCELLULAR LOCATION: Exists as a type I membrane protein and as a
CC proteolytically released soluble growth factor form. The membrane-
CC bound form does not seem to be active (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Comment=Additional isoforms seem to exist;
CC Name=1; Synonyms=ARIA, IG-NRG;
CC IsoId=Q05199-1; Sequence=Q05199-1; Sequence=Displayed;
CC Note=Contains an Ig-like domain;
CC Name=2; Synonyms=CRD-NRG-BETA1A;
CC IsoId=Q05199-2; Sequence=VSP_003445;
CC Note=The EGF-like domain is replaced by a Cysteine-rich domain
CC (CRD);
CC Name=3; Synonyms=CRD-NRG-BETA2A;
CC IsoId=Q05199-3; Sequence=VSP_003445; VSP_003446;
CC Note=The EGF-like domain is replaced by a Cysteine-rich domain
CC (CRD);
CC Name=4; Synonyms=CRD-NRG-BETA2B;
CC IsoId=Q05199-4; Sequence=VSP_003445; VSP_003446; VSP_003447;
CC Note=The EGF-like domain is replaced by a Cysteine-rich domain
CC (CRD);
CC -1- DEVELOPMENTAL STAGE: Isoforms 2-4 are detected at embryonic day 4
CC (ED4) in both visceral and somatic motor neurons of spinal cord
CC and is highest at ED6. Isoform 1 is not expressed until ED 6 in
CC spinal cord. At ED 11 both isoforms display comparable levels
CC -1- DOMAIN: The cytoplasmic domain may be involved in the regulation
CC of trafficking and proteolytic processing. Regulation of the
CC proteolytic processing involves initial intracellular domain
CC dimerization (By similarity).
CC -1- DOMAIN: ERBB receptor binding is elicited entirely by the EGF-like
CC domain.
CC -1- PM: Proteolytic cleavage close to the plasma membrane on the
CC external face leads to the release of the soluble growth factor
CC form.
CC -1- PM: Extensive glycosylation precedes the proteolytic cleavage (By
CC similarity).
CC -1- SIMILARITY: Contains 1 EGF-like domain.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -1- SIMILARITY: Belongs to the neu-regulin family.
CC -----
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CC -----
CC EMBL; L11264; AAA49037.1; --
CC EMBL; AF045654; AAC05670.1; --
CC EMBL; AF045655; AAC05671.1; --
CC EMBL; AF045656; AAC05672.1; --
CC PIR; A45769; A45769.
CC HSSP; Q12784; 1HRE.
CC InterPro; IPR006209; EGF_like.
CC InterPro; IPR006210; IEGF.

```

CC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALEB/GJ;
 RX MEDLINE=89279149; PubMed=2499654;
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 the primary immune response";
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
 DR PIR; J0507; HVMS39.
 DR HSSP; P01810; 2FEJ.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG-LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 7-39.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON TER 117 117
 SQ SEQUENCE 117 AA; 12972 MW; D5CA4167D0F1774F CRC64;
 Query Match 14.8%; Score 57.5; DB 1; Length 117;
 Best Local Similarity 38.2%; Pred. No. 4.3; Mismatches 9; Indels 5; Gaps 2;
 Matches 13; Conservative 7;
 QY 29 KTPKTKYXSLRW-KKLGSRVSFVYQTLQGF 61
 DB 58 QTPEK---RLEWVASISGGVSYTYPSYKGRF 87
 RESULT 13
 ID RUVB RHET STANDARD; PRT; 346 AA.
 AC Q9L9G3;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Holliday junction DNA helicase ruvb.
 GN RUVB.
 OS Rhizobium etli.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
 OX NCBI_TaxID=29449;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CE3;
 RX MEDLINE=20156376; PubMed=10675620;
 RA Martinez-Salazar J.M., Romero D.;
 RT "Role of the ruvB gene in homologous and homeologous recombination in
 Rhizobium etli";
 RL Gene 243.125-131(2000).
 CC -1- FUNCTION: the ruvA-ruvB complex in the presence of ATP renatures
 cruciform structure in supercoiled DNA with palindromic sequence,
 indicating that it may promote strand exchange reactions in
 homologous recombination. RuvAB is an helicase that mediates the
 Holliday junction migration by localized denaturation and
 reannealing (By similarity).
 CC -1- SUBUNIT: Forms a complex with ruvA (By similarity).
 CC -1- SIMILARITY: Belongs to the ruvB family.
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 or send an email to license@isb-sib.ch).
 EMBL; U13645; AAA20987.2; -
 HSSP; P24941; 1HCL.
 DR WormPep; C05D10.2; CE29020.
 DR InterPro; IPR003527; MAP kin.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
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 or send an email to license@isb-sib.ch).
 EMBL; AF175525; AAF36814.1; -
 DR HAMAP; MF_00016; -; 1.
 DR InterPro; IPR003593; AAA ATPase.
 DR InterPro; IPR003959; AAA ATPase_cent.
 DR InterPro; IPR004605; RuvB.
 DR InterPro; IPR008823; RuvB_C.
 DR InterPro; IPR008824; RuvB_N.
 DR Pfam; PF00004; AAA; 1.
 DR Pfam; PF05491; RuvB_C; 1.
 DR Pfam; PF05496; RuvB_N; 1.
 DR SMART; SM00382; AAA; 1.
 DR TIGRFAMs; TIGR00635; ruvB; 1.
 KW DNA repair; SOS response; ATP-binding; DNA recombination; Helicase.
 FT NP_BIND 60 67
 SQ SEQUENCE 346 AA; 38462 MW; 55EB3E4D3A273BEC CRC64;
 Query Match 14.8%; Score 57.5; DB 1; Length 346;
 Best Local Similarity 29.5%; Pred. No. 14;
 Matches 13; Conservative 10; Mismatches 18; Indels 3; Gaps 2;
 QY 4 AYGFSAFQD--QQVTAIXYQEAFLACKTPKTKYXSLRWKLG 45
 DB 285 AAGLSEPRDAIEDIEPYMIQQGFQ-RTPGRVLTATAWKHLG 327
 RESULT 14
 ID YPC2 CABEL STANDARD; PRT; 470 AA.
 AC Q11179;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Putative serine/threonine-protein kinase C05D10.2 in chromosome III
 (EC 2.7.1.37).
 GN C05D10.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Du 2.;
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP REVISIONS.
 RA Waterston R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- COFACTOR: Magnesium (By similarity).
 CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. MAP
 kinase subfamily.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 EMBL; U13645; AAA20987.2; -
 HSSP; P24941; 1HCL.
 DR WormPep; C05D10.2; CE29020.
 DR InterPro; IPR003527; MAP kin.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.

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DR SMART, SMC0220; S_TKC; 1.
DR PROSITE; PS01351; MAPK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Hypothetical protein; transferase; Serine/threonine-protein kinase;
FT CHAIN 13 306 PROTEIN_KINASE.
FT NP_BIND 19 27 ATP (BY SIMILARITY).
FT BINDING 42 42 ATP (BY SIMILARITY).
FT ACT_SITE 137 137 BY SIMILARITY.
SQ SEQUENCE 470 AA; 54038 MW; 8908849D15173DF0 CRC64;

Query Match 14.8%; Score 57.5; DB 1; Length 470;
Best Local Similarity 26.9%; Pred. No. 20;
Matches 21; Conservative 13; Mismatches 39; Indels 5; Gaps 2;

QY 3 KAYG-TSAPKQQQVAVVAVYQEAAILACKTPK----KVXSRLEWKKLGRSVFVYQQTL 57
DB 75 KLYNIFRADNRDIYLAFEWEADLNHVIKGSILKDVHKQYIMCOLFRAIRLHSGNVL 134
QY 58 QGDFKRAEMIDFNIRIK 75
DB 135 HRDLKPSNVLLDADCRVK 152

RESULT 15
HA70_CLOBO STANDARD; PRT; 623 AA.
AC P46085;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Hemagglutinin components HA-53 and HA-22/23 precursor.
GN HA-70 OR ANTP-70.
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Type C Stockholm / C-ST / 468;
RX MEDLINE=94301293; PubMed=8028579;
RA Hauser D.F., Eklund M.W., Boquet P., Popoff M.R.;
RT "Organization of the botulinum neurotoxin C1 gene and its associated
RL non-toxic protein genes in Clostridium botulinum C 468.";
RL Mol. Genet. 243:631-640(1994).
CC [-] SUBUNIT: HA IS COMPOSED OF SUBCOMPONENTS HAVING 53, 33, 22-23, AND
CC 17 kDa. BOTULINUM TOXINS ARE PRODUCED AS PROGENITOR TOXINS OF
CC LARGE MOLECULAR SIZES OF 12S (M TOXIN), 16S (L TOXIN) AND 19S (LL
CC TOXIN). M TOXIN CONSISTS OF A NONTOXIC COMPONENT AND THE
CC NEUROTOXIN. L TOXIN CONSISTS OF THE M TOXIN AND HA.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D38562; BAA07575.1; -
CC EMBL; S74768; AAB32849.1; -
CC EMBL; X72793; CAA51309.1; -
```

```
DR InterPro; IPR003897; Clenterotox.
DR Pfam; PF03505; Clenterotox; 2.
DR PRINTS; PR01394; CLENTERTOXN.
KW Hemagglutinin. 7 192 HEMAGGLUTININ COMPONENT HA-23A
FT CHAIN 10 192 (POTENTIAL).
FT CHAIN 13 192 HEMAGGLUTININ COMPONENT HA-23B
FT CHAIN 15 192 (POTENTIAL).
FT CHAIN 193 623 HEMAGGLUTININ COMPONENT HA-22B
FT CHAIN 623 623 HEMAGGLUTININ COMPONENT HA-53.
SQ SEQUENCE 623 AA; 70649 MW; 115FFB1B2F3FB667 CRC64;

Query Match 14.8%; Score 57.5; DB 1; Length 623;
Best Local Similarity 42.9%; Pred. No. 27;
Matches 12; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

QY 49 SFVYQQTLQGDFFKNRAEMIDFNIRIK 76
DB 532 NYISYQLTIPGDFNFIASSI-FSPRTN 558

Search completed: July 15, 2004, 23:53:12
Job time : 4.25134 secs
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2004, 23:49:33 ; Search time 13.4118 seconds
(without alignments)
1787.936 Million cell updates/sec

Title: US-09-852-797-76_COPY_23_98
Perfect score: 388
Sequence: 1 YHKAYGSAFKDQOVTVAVX.....LQGFKNRAEMIDNIRIKN 76

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mmc: *
8: sp_organelle: *
9: sp_phase: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriaph: *
17: sp_archaea: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	307.5	79.3	181	11 Q9CWD9	Q9cwd9 mus musculus
2	307.5	79.3	298	11 Q9J159	Q9j159 mus musculus
3	307.5	79.3	298	11 Q8CE95	Q8ce95 mus musculus
4	307.5	79.3	298	11 Q8CEK9	Q8cek9 mus musculus
5	80	20.6	309	4 Q96P11	Q96f11 homo sapien
6	80	20.6	310	4 Q9BX67	Q9bx67 mus musculus
7	80	20.6	355	4 Q8WNL8	Q8w18 homo sapien
8	74.5	19.2	310	11 Q9DBB7	Q9dbb7 mus musculus
9	74.5	19.2	310	11 Q9DLM9	Q9dlm9 mus musculus
10	74.5	19.2	310	11 Q9EPK4	Q9epk4 mus musculus
11	72.5	18.7	437	16 Q8EZ10	Q8ez10 leptospira
12	71	18.3	300	13 Q7SVQ7	Q7svq7 xenopus lae
13	68	17.5	4440	5 Q8I5W6	Q8i5w6 plasmodium
14	67.5	17.4	641	17 Q970A5	Q970a5 sulfolobus
15	67	17.3	289	13 Q7ZWTO	Q7zwto xenopus lae
16	66	17.0	157	2 Q52245	Q52245 enterococcu

17	66	17.0	322	2 Q8L1C7	Q8l1c7 enterococcu
18	65	16.8	275	15 Q8RVV7	Q8rvv7 thermoaer
19	63.5	16.4	275	13 Q8AVV1	Q8avv1 xenopus lae
20	62.5	16.1	424	16 Q83EU4	Q83ej4 coxiella bu
21	62.5	16.1	573	15 Q8DBY7	Q8db7 vibrio vuln
22	62	16.0	231	2 Q4941	Q54941 streptococc
23	62	16.0	374	16 Q8F2R9	Q8f2r9 leptospira
24	62	16.0	461	10 Q84RH9	Q84rh9 chlorarachn
25	60.5	15.6	188	15 Q8Z1O8	Q8z1o8 salmonella
26	60	15.5	124	16 Q92FV6	Q92fv6 rickettsia
27	60	15.5	214	16 Q7VR53	Q7vr53 candidatus
28	60	15.5	733	5 Q8SWD6	Q8swd6 encephalito
29	59.5	15.3	271	16 Q7VGU7	Q7vgu7 helicobacte
30	59.5	15.3	318	10 Q8LAY7	Q8lay7 arabidopsis
31	59.5	15.3	414	16 Q8UDV4	Q8udv4 agrobacteri
32	59.5	15.3	444	16 Q8Z7H5	Q8z7h5 salmonella
33	59.5	15.3	803	16 Q9ZJV3	Q9zjv3 helicobacte
34	59.5	15.3	1009	16 Q8XMB8	Q8xmb8 clostridium
35	59.5	15.3	1100	3 Q8X1U2	Q8x1u2 penicillium
36	59	15.2	255	2 Q848Y3	Q848y3 bacillus me
37	59	15.2	433	13 Q91859	Q91859 xenopus lae
38	59	15.2	438	11 Q9JLB7	Q9jlb7 mus musculu
39	59	15.2	510	11 Q9JLB8	Q9jlb8 mus musculu
40	59	15.2	549	11 Q9D006	Q9d006 mus musculu
41	59	15.2	549	11 Q9JLB9	Q9jlb9 mus musculu
42	59	15.2	551	5 Q94760	Q94760 strongyloce
43	58.5	15.1	301	16 Q92BC7	Q92bc7 listeria in
44	58.5	15.1	333	16 Q8YUV3	Q8yuv3 anabaena sp
45	58.5	15.1	491	5 Q8SVY4	Q8svy4 encephalito

ALIGNMENTS

RESULT 1
Q9CWD9 PRELIMINARY; PRT; 181 AA.
ID Q9CWD9
AC Q9CWD9; (TREMELrel. 17, Created)
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DE 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE 2410167M24Rik protein (Junction cell adhesion molecule 2).
GN JAM2 OR JCM2 OR 2410167M24RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryonic stem cells;
RX MEDLINE=21085860; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbets P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kotsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [2]
RP SEQUENCE FROM N.A.

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RC STRAIN=C57BL/6J;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK010826; BAB27208.1; -.
DR EMBL; AK045095; BAC32219.1; -.
DR MGD; MGI:1933820; Jam2.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG LIKE; 1.
SQ SEQUENCE 181 AA; 20330 MW; 603B6114FBB11AEB CRC64;

Query Match 79.3%; Score 307.5; DB 11; Length 181;
Best Local Similarity 77.9%; Pred. No. 2e-30;
Matches 60; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 1 YHKYGFSA PKD-QQVTVAVXYQAEAILACKTPKKTVXSRLEWKKLGRSVFVYQQTLOG 59
DB 23 YHKANGFSAS KDHQREVTVIEFQAEAILACKTPKKTTSRLWKVGGVSLVYQQALQG 82

QY 60 DFKRAEMIDFNIRIKN 76
DB 83 DFKRAEMIDFNIRIKN 99

RESULT 2
QJUI59 PRELIMINARY; PRT; 298 AA.
AC QJUI59;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 25, Last annotation update)
DE Vascular endothelial junction-associated molecule (Junctional adhesion
DE molecule-3) (2410030G21Rik protein).
GN JAM2 OR JCAM3 OR JCAM2 OR JAM-3 OR 2410030G21Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=20317114; PubMed=10779521;
RA Palmeri D., van Zante A., Huang C.-C., Hemmerich S., Rosen S.D.;
RT "Vascular Endothelial Junction-associated Molecule, a Novel Member of
RT the Immunoglobulin Superfamily, Is Localized to Intercellular
RT Boundaries of Endothelial Cells.";
RL J. Biol. Chem. 275:19139-19145 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RX PubMed=11036763;
RA Aurand-Lions M.A., Duncan L., Du Pasquier L., Imhof B.A.;
RT "Cloning of JAM-2 and JAM-3: an Emerging Junctional Adhesion Molecular
RT Family?";
RL Curr. Top. Microbiol. Immunol. 251:91-98 (2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo, and Embryonic stem cells;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischman W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boifelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

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RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
DR EMBL; AF255911; AAF81224.1; -.
DR EMBL; AJ291757; CAC20699.1; -.
DR EMBL; AK013914; BAB29053.1; -.
DR EMBL; AK010616; BAB27064.1; -.
DR MGD; MGI:1933820; Jam2.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 2.
DR PROSITE; PS00835; IG LIKE; 2.
SQ SEQUENCE 298 AA; 33047 MW; 1124E0F07E6CF751 CRC64;

Query Match 79.3%; Score 307.5; DB 11; Length 298;
Best Local Similarity 77.9%; Pred. No. 3.4e-30;
Matches 60; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 1 YHKYGFSA PKD-QQVTVAVXYQAEAILACKTPKKTVXSRLEWKKLGRSVFVYQQTLOG 59
DB 23 YHKANGFSAS KDHQREVTVIEFQAEAILACKTPKKTTSRLWKVGGVSLVYQQALQG 82

QY 60 DFKRAEMIDFNIRIKN 76
DB 83 DFKRAEMIDFNIRIKN 99

RESULT 3
Q8CE95 PRELIMINARY; PRT; 298 AA.
ID Q8CE95;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Junction cell adhesion molecule 2.
GN JAM2 OR JCAM2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK028757; BAC26102.1; -.
DR MGD; MGI:1933820; Jam2.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
SQ SEQUENCE 298 AA; 33079 MW; CB8227EC13D349A3 CRC64;

Query Match 79.3%; Score 307.5; DB 11; Length 298;
Best Local Similarity 77.9%; Pred. No. 3.4e-30;
Matches 60; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 1 YHKYGFSA PKD-QQVTVAVXYQAEAILACKTPKKTVXSRLEWKKLGRSVFVYQQTLOG 59

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DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 2.
DR PROSITE; PS00835; IG_LIKE; 2.
KW Hypothetical protein; Signal.
FT SIGNAL 1 30
SQ SEQUENCE 310 AA; 35020 MW; CE39ADF33EALDAB9 CRC64;

Query Match 20.6%; Score 80; DB 4; Length 310;
Best Local Similarity 32.0%; Pred. No. 0.12;
Matches 16; Conservative 13; Mismatches 19; Indels 2; Gaps 2;

QY 21 YQEAAILAC-KTPKTVXSRLEWKKL-GRSVSFVYQQTLQGFKNRAEMI 68
DB 46 FESVELSCIITDSQTSDFRIEWKKIQDEQTYVFFDNKIQDLAGRAEIL 95

RESULT 7
Q8WVL8 PRELIMINARY; PRT; 355 AA.
AC Q8WVL8
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Junction adhesion molecule 3.
GN JAM3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RA Hearn T.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN 2
RP SEQUENCE FROM N.A.
RA Phillips H.M.;
RT "Narrowing the critical region within liq24-qter for hypoplastic left heart and identification of a candidate gene, JAM3, expressed during cardiogenesis.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ416101; CAC94776.1; -.
DR Genew; HGNC:15532; JAM3.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
KW Immunoglobulin domain.
FT CHAIN 76 355 JUNCTION ADHESION MOLECULE 3.
SQ SEQUENCE 355 AA; 39602 MW; 8B1577DEA7B1D4F8 CRC64;

Query Match 20.6%; Score 80; DB 4; Length 355;
Best Local Similarity 32.0%; Pred. No. 0.14;
Matches 16; Conservative 13; Mismatches 19; Indels 2; Gaps 2;

QY 21 YQEAAILAC-KTPKTVXSRLEWKKL-GRSVSFVYQQTLQGFKNRAEMI 68
DB 91 FESVELSCIITDSQTSDFRIEWKKIQDEQTYVFFDNKIQDLAGRAEIL 140

RESULT 8
Q9DB87 PRELIMINARY; PRT; 310 AA.
AC Q9DB87
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 1110002N23RIK protein.
GN JCAM3 OR JCAM2 OR 1110002N23RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

[1]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald I., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Tovo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kotsuki S., Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK008187; BAB25519.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
KW Immunoglobulin domain.
SQ SEQUENCE 310 AA; 34855 MW; C74884EABE234680 CRC64;

Query Match 19.2%; Score 74.5; DB 11; Length 310;
Best Local Similarity 30.5%; Pred. No. 0.58;
Matches 18; Conservative 14; Mismatches 24; Indels 3; Gaps 3;

QY 21 YQEAAILAC-KTPKTVXSRLEWKKL-GRSVSFVYQQTLQGFKNRAEMI-DFNIRKN 76
DB 46 FESVELSCIITDSQTSDFRIEWKKIQDQTYVFFDNKIQDLAGRTDVFCKTSLRN 104

RESULT 9
Q9DIM9 PRELIMINARY; PRT; 310 AA.
AC Q9DIM9
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 1110002N23RIK protein.
GN JCAM3 OR JCAM2 OR 1110002N23RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

[1]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
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RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kontsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK003326; BAB22715.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_C2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR Immunoglobulin domain.
SQ SEQUENCE 310 AA; 34819 MW; 6692BCAD68EA4B1D CRC64;

Query Match 19.2%; Score 74.5; DB 11; Length 310;
Best Local Similarity 30.5%; Pred. No. 0.58; 24; Indels 3; Gaps 3;
Matches 18; Conservative 14; Mismatches 24; Indels 3; Gaps 3;

QY 21 YQEAIALAC-KTPKKTXXSRLEWKKL-GRSVSFVYQQTLOGDFKNRAEMI-DFNIRIKN 76
Db 46 FESVELSCIITDSQSDPRIEWKKIQDQTTVYVFDNKIQGLAGRTDVFGKTSLRWN 104

RESULT 10
Q9EPK4 PRELIMINARY; PRT; 310 AA.
AC Q9EPK4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Functional adhesion molecule-2, JAM-2 (1110002N23Rik protein)
DE (Junction cell adhesion molecule 3).
DE JAM3 OR JCAM3 OR JCAM2 OR JAM-2 OR 1110002N23RIK.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PubMed=11036763;
RX Aurrand-Lions M.A., Duncan L., Du Pasquier L., Imhof B.A.;
RA "Cloning of JAM-2 and JAM-3: an Emerging Functional Adhesion Molecular
RT Family?";
RL Curr. Top. Microbiol. Immunol. 251:91-98(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirral L.M., Staebli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Anon H., Baldarelli R., Barsh G.,
RA Blake J., Bojelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kontsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX Strausberg R.;

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RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mesonephros;
RX MEDLINE=22354683; PubMed=12466851;
RA the FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573(2002).
DR EMBL; AJ300304; CAC20704.1; -.
DR EMBL; AK013156; BAB28683.1; -.
DR EMBL; BC024357; AAH24357.1; -.
DR EMBL; AK032833; BAC28049.1; -.
DR MGD; MGI:1933825; Jam3.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_C2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR Immunoglobulin domain.
SQ SEQUENCE 310 AA; 34837 MW; 4B92BCB51D0A4B0A CRC64;

Query Match 19.2%; Score 74.5; DB 11; Length 310;
Best Local Similarity 30.5%; Pred. No. 0.58; 24; Indels 3; Gaps 3;
Matches 18; Conservative 14; Mismatches 24; Indels 3; Gaps 3;

QY 21 YQEAIALAC-KTPKKTXXSRLEWKKL-GRSVSFVYQQTLOGDFKNRAEMI-DFNIRIKN 76
Db 46 FESVELSCIITDSQSDPRIEWKKIQDQTTVYVFDNKIQGLAGRTDVFGKTSLRWN 104

RESULT 11
Q8EZ10 PRELIMINARY; PRT; 437 AA.
AC Q8EZ10;
DT 01-VAR-2003 (TrEMBLrel. 23, Created)
DT 01-VAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Conserved hypothetical protein.
DE Leptospira interrogans.
OS Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]_TaxID=173;
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RA Ren S.;
RX Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE011560; AAN51249.1; -.
DR InterPro; IPR005532; DUF323.
DR Pfam; PF03781; DUF323; 1.
DR KX Hypothetical protein; Complete proteome.
SQ SEQUENCE 437 AA; 49999 MW; CFA258D01D54C527 CRC64;

Query Match 18.7%; Score 72.5; DB 16; Length 437;
Best Local Similarity 23.8%; Pred. No. 1.5;
Matches 20; Conservative 17; Mismatches 32; Indels 15; Gaps 2;

QY 3 KAYGSAPKDDQVAVTAVYQEAIALACKTPKKTXXSRLEWK-----KLGRSVSFVY 52
Db 257 KSGNFPAGKEHPVSGITYREAETVARMWKGKLPTEMEWEKKAARGTGMWTKINRDESYSF 316

QY 53 YQQTLOGDFKNRAEMIDFNIRIKN 76
Db 317 FPSPLEYFPGN-----DFDSTLCN 335

RESULT 12
Q7SYQ7 PRELIMINARY; PRT; 300 AA.
AC Q7SYQ7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)

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OS	Plasmodium falciparum (isolate 3D7).
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX	NCBI_TaxID=36329;
[1]	RN
RP	SEQUENCE FROM N.A.
RC	STRAIN=3D7;
RX	MEDLINE=2255705; PubMed=12368864;
RA	Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA	Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA	Bisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA	Chan M.-S., Nene V., Shellenom S.J., Suh B., Peterson J., Angiuoli S.,
RA	Pertea M., Allen J., Sellout G.J., Haft D., Mather M.W., Vaidya A.B.,
RA	Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA	McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA	Venter J.C., Carucci D.J., Hoffman S.D., Newbold C., Davis R.W.,
RA	Fraser C.M., Barrrell B.;
RT	"Genome sequence of the human malaria parasite Plasmodium
RT	falciparum.";
RL	Nature 419:498-511(2002).
RL	EMBL; AB014845; BAN36170.1; -.
KW	Hypothetical protein.
DQ	SEQUENCE 4440 AA; S30139 MW; BD9394A01FB84FD9 CRC64;
SQ	
Query Match	17.5%; Score 68; DB 5; Length 4440;
Best Local Similarity	27.1%; Pred. No. 74;
Matches	26; Conservative 13; Mismatches 37; Indels 20; Gaps 4;
QY	1 YHKAYGFSAPKDDQ--QVVTAXYQAAILACKTPKTVXSL--EWMKLGRS----- 47
DB	1092 HFKKNYIENDXRIFKVATKFVFSEIIIMLNPLVTPKAIVDVRKKYLRTFSNNHDINS 1151
QY	48 ----VSFVVYQQTLOGDFKN---RAEMIDFNIRIKN 76
DB	1152 NRDDSFDFYFVVCNCFKNSRKKDMIEYNLKN 1187
RESULT 14	
Q970A5	PRELIMINARY; PRT; 641 AA.
ID	Q970A5
AC	Q970A5
DT	01-DEC-2001 (TRENDELrel. 19, Created)
DT	01-DEC-2001 (TRENDELrel. 19, Last sequence update)
DT	01-JUN-2003 (TRENDELrel. 24, Last annotation update)
DE	Putative hydatoin utilization protein.
GN	ST1686.
OS	Sulfolobus tokodaii.
OC	Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC	Sulfolobus.
OX	NCBI_TaxID=111955;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=JCM 10545 / 7;
RX	MEDLINE=21456156; PubMed=11572479;
RA	Kawarayashi Y., Hino Y., Horikawa H., Jin-no K., Takabashi M.,
RA	Sekine Y., Baba S.-I., Ankaï A., Kosugi H., Hosoyama A., Fukui S.,
RA	Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA	Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA	Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA	Oshima T., Kikuchi H.;
RT	"Complete genome sequence of an aerobic thermoacidophilic
RT	Crenarchaeon, Sulfolobus tokodaii strain?";
RL	DNA Res. 8:123-140(2001).
DR	EMBL; AP000987; BAB66768.1; -.
DR	GO; GO:0016787; F:hydrolase activity; IEA.
DR	InterPro; IPRO02821; Hydantoinase_A.
DR	InterPro; IPRO08040; Hydantoinase_A.
DR	Pfam; PF01968; Hydantoinase_A.1.
DR	Pfam; PF05378; Hydantoinase_A.1.
KW	Hypothetical protein; Complete proteome.
SQ	SEQUENCE 641 AA; 71166 MW; Q29C34CFB4A6841 CRC64;
Query Match	17.4%; Score 67.5; DB 17; Length 641;
Best Local Similarity	29.3%; Pred. NO. 9.8;

Search completed: July 15, 2004, 23:54:30
Job time : 14.4118 secs

